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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:07:09 ; Search time 22.5 Seconds (without alignments) 100.734 Million cell updates/sec Run on:

AUDET-909-1 52

1 eevvpAgmsys 11 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL Database

sp\_archea:\*
sp\_bacteria:\*
sp\_fung1:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_morgane1le:\*
sp\_phage:\*

\*pplant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_rvirus:\*
sp\_bacteriap:\* sp archeap:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ				
Result No.	Score		Query Match Length DB	DB	ID	Description
н	38	73.1	387	16	Q98FX1	O98fx1 rhizobium
	38	73.1	1063	16	Q8RG86	OBrq86 fusobacteri
3	38	73.1	3472	1	074056	074056 cenarchaeum
4	37	71.2	840	٣	Q9URY8	Ogury8 schizosacch
Ŋ	36	69.2	471	11	O8R126	O8r126 mus musculu
9	36	69.2	484	11	Q8VD18	O8vd18 mus musculu
7	35	67.3	225	10	040129	040129 lycopersico
89	35	67.3	425	2	Q9XVK4	09xvk4 caenorhabdi
6	35	67.3	556	4	043733	043733 homo sapien
10	35	67.3	583	Ŋ	Q9BHA5	O9bha5 plasmodium
11	35	67.3	583	Ŋ	09вн83	09bh83 plasmodium
12	35	67.3	670	11	001487	001487 rattus norv
13	35	67.3	749	16	09PDM6	Ogodm6 xvlella fas
14	35	67.3	1902	4	Q14122	Q14122 homo sapien
15	34	65.4	156	m	Q12479	012479 saccharomyc
16	34	65.4	219	17	097182	Q971s2 sulfolobus

	Q9fnl4 arabidopsis Q9x0u3 thermotoga Q9v914 drosophila Q96csO homo sapien Q94csy mus musculu Q8r8k6 thermoanaer Q96mb2 homo sapien
028342 096MU1 0998DD 098BP5 098PP5 098TT05 098TT05 098TT05 098TT05 098TT05 098TT05 098TT05 098TT05 098TT05 099000 099000 0990000 099000 099000	Q9FNL4 Q9X0U3 Q9V914 Q96CS0 Q9D2X9 Q8R8K6
7 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	10 14 11 16 16
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1117 12000000000000000000000000000000000	0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

### ALIGNMENTS

[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S., Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."; Gaps 096FX1; 01-OCT-2001 (TEMBLE). 18, Created) 01-OCT-2001 (TEMBLE). 18, Last sequence update) 01-OCT-2001 (TEMBLE). 18, Last annotation update) Hippurate hydrolase. MIR\$583. Rhizobium loti (Mesorhizobium loti). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; .. 0 73.1%; Score 38; DB 16; Length 387; 60.0%; Pred. No. 9.8; ative 2; Mismatches 2; Indels DNA Res. 7:331-338(2000).

EMBL; AP003002; BAB50445.1; -.

InterPro; IPR002933; Peptidase M20.

Pfam; PF01546; Peptidase M20; Ī.

Hydrolase; Complete protecome.

SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64; 387 AA. PRT; PRELIMINARY; Conservative Query Match Best Local Similarity NCBI\_TaxID=381; 9 Q98FX1 RESULT 1 098FX 

:| :| |||| 367 DEAIPHGMSY 376 1 EEVVPXGMSY 10 g Š

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audet-909-1.rspt

|:|:| |:|:| 2294 EDVIPRGISFS 2304

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RESULT 2

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2 EVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                    3 VVPXGMSYS 11
                                                                                                                                                                           Schizosaccharomyces.
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                       NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
                                                                                                                        SPAC869.05C.
                                                          Q9URY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8R126
                                              Q9URY8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
Q8R126
                      RESULT 4
                                  Q9URY8
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J. Bacteriol. 180:5003-5009(1998).

-! SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOWAINS).

EMBL; AF083072; AAC62699.1; -.

InterPro; IPRO00515; BPD transp.

InterPro; IPRO01680; WD40.

Ffam; PF00400; WD40; 4.

SMART; SM00320; WD40; 2.

PROSITE; PS00402; BPD TRANSP_INN_MEMBR; UNKNOWN_1.

Hypothetical protein; Repeat: WD repeat.

SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                            STRAIN-ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpidas N., Overbeek R.;
Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
Bigse; Complete proteome.
SEQUENCE 1063 AA, 118008 MW; 39700E10B7CCE411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   0;
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Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                          73.1%; Score 38; DB 16; Length 1063; 60.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.1%; Score 38; DB 1; Length 3472; 54.5%; Pred. No. 1e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                               01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 3472 AA
          PRT; 1063 AA
                                                                                                  Fusobacterium nucleatum (subsp. nucleatum).
                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                            Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
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Archaea; Crenarchaeota; Cenarchaeum.
                                     Created)
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Hypothetical 367.1 kDa protein.
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Best Local Similarity 54.5.
Best Local Similarity 6.5.
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60...
6, Conservative
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                       Q8RG86;
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                             |:|| |::||
195 EIVPNGLNYS 204
                                                                                                                                                                                                                                                                                                                                                                                               2 EVVPXGMSYS 11
                                                                                                                                                  FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=B;
                                                                                                                                                  SEQUENCE
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           08RG86
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074056
OBRG86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                       STRAIN=972H-;
STRAIN=972H-;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Ali32779; CABGOUS-1; -.
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
Pfam; PF01740; STAS; I.
Pfam; PF00916; Sulfate_transp; 1.
TIGRFAMS; TIGR00815; sulfate_transp; 1.
SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%; Score 37; DB 3; Length 840; 77.8%; Pred. No. 37; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC025810; AAH25810.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NÖN TER 1 1
SEQÜENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;
                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBR126;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54.5 kDa protein (Fragment).
Mus musculus (Mouse).
                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
probable sulfate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 AA.
840 AA
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PRT;
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Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%
---- 7; Conservative
  PRELIMINARY;
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RESULT 6

Q8VD18

1 EEVVPXGMSYS 11

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Q8VD18;

08VD18

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Eukaryota; Mecazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.3%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 48; tive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tubby B.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Z98050; CAB10847.1;
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                            Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
EMBL, 281109; CAB03241.1;
InterPro; IPR000719; Euk pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Buk pkinase; 1.
PROSITE; PS500011; PROFINIKINASE_DOM; 1.
SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BHA5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 AA.
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA binding protein (Fragment).
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nes 5; Conservative
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244 VVPAGLTYS 252
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                                                                                                                                              R10D12.10. -
Caenorhabditis elegans
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                                                                                                                R10D12.10 protein.
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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Matches
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
1-ycopersicon esculentum (Tomato).
1-ycopersicon esculentum (Tomato).
1-ycopersicon seculentum (Tomato).
1-ycopersicon esculentum (Tomato).

                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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STRAIN=VP36; TISSUE=PISTIL;
MEDLINE=5937523; PubMed=7647301;
Milligan S.B., Gasser C.S.;
Milligan S.B., Gasser C.S.;
Plant Mol. Biol. 28:691-711(1995).
EMBI, U20592; AAA80497.1;
InterPro; IPR002160; Kunitz_legume.
Fram; PP000197; Kunitz_legume; 1.
ProDom; PD000891; Kunitz_legume; 1.
SVART; SM00642; STI; 1.
SVART: SM06452; STI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 36; DB 11; Length 484; 60.0%; Pred. No. 33; tive 2; Mismatches 2; Indels
                                                                              01-WAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017637; AAH17637.1; -.
EMBL; MR12128595; AWR36441.
SEQUENCE 484 AA; SE835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 225 UNKNOWN.
225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PS00283; SÓYBEAN KUNITZ, UNKNOWN 1.
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 AA
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              484 AA
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              PRT;
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Best Local Similarity 60.07
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              PRELIMINARY;
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239 EVIPAGASYN 248
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TISSUE=SALIVARY GLAND;
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Best Local Similarity
Matches 6; Conserva
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NCBI_TaxID=2371;
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Q9PDM6
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                        Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;
Plasmodium falciparum choline transporter (PfSCT1) gene.";
Submitted (AuG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AX007372; AAK14816.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;

Plassmodium falciparum choline transporter (PfSCTI) gene.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AY007374; AAK14818.1;

EMBL; AY007373; AAK14817.1;

EMBL; AY0071373; AAK14817.1;

EMBL; AY0071373; ACY1transferase.

Pfam; PF01553; ACY1transferase; 1.

SRQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;
                                                                                                                                                                                                                                                                                                                                     67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67; 1:ve 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%; Score 35; DB 5; Length 583; 55.6%; Pred. No. 67;
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                                                                                                                                                                                                                                  EMBL; AY007375; AAG17947.1; -
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66917 MW; 2B2BFAE3E395E049 CRC64;
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Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                     55.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                           Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                 3 VVPXGMSYS 11
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Plasmodium falciparum.
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                    Choline transporter.
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Best Local Similarity
                                                                                                                                       SEQUENCE FROM N.A.
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barcos M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Calutco M.R.D., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Colutio L.L., Cristofani M., Dias.Neto E., Docena C., El-Dorry H., Farga J.S., Ferreira V.C.A., Ferro J.A., Ferreira A.J.S., Ferreira W., Fornon I.R., Goldman M.H., S., Gomes S.L., Gruber A., A. Garnier M., Goldman G.H., Goldman M.H., Kemper E.L., Kitajima J.P., Nrieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos B.G.M., Madeira A.M.B.N., Madeira H.M.F., Martino C.L., Marques M.V., Martins E.M.F., Matsukuma A.Y.,
                                             InterPro; IPR000822; Znf_C2H2.
Pfam, PF00096; zf-C2H2; 2.
SMART; SM00355; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS0197; ZNC_FINGER_C2H2_2; 2.
Zinc-finger; Nuclear protein, DNA-binding; Transcription regulation; Metal-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: HIGHLY SIMILAR TO AT-BP1 AND TO THE PRDII-BF1 FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- MISCELLANEOUS: ACIDIC AMINO ACID REGION MAY BE INVOLVED IN TRANSCRIPTIONAL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%; Score 35; DB 11; Length 670; 66.7%; Pred. No. 78; 1:ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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C(2)H(2) CLASS.
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STRAIN=SPRAGUE-DAWLEY; TISSUE=THYROID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20365717; PubMed=10910347;
                        MEDLINE=91187610; PubMed=1901405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X54250; CAA38151.1; -. HSSP; P15822; 1BBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 6; Conservative
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104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          670 AA;
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156 AA

PRELIMINARY;

Q12479; 012479 RESULT 15 012479

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Menck C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A. de Oliveira M.C., ede Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Quagqio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
de Rosa V.E. Jr., da Silva M.M., da Silva F.R., Silva M.A. Jr.,
da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Jr.,
da Silva A.C.R., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
de Souza A.P., Terenti M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A. Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
M. Rembi, AE003967; AAF84162.1; -.
REMBL; AE003967; AAF84162.1; -.
REMBL; AE003967; AAF84162.1; -.
REMBL; AE003967; DNA topoisolV, 1.
Rembro, IPRO02205; DNA topoisolV, 1.
Rembro, ROMAL, C. M. A. DODISOLV, 1.
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A MEDILINE-90205817; PubMed=2108316;
A Baldwin A.S., LeClair K.P., Singh H., Sharp P.A.;
Baldwin A.S., LeClair K.P., Singh H., Sharp b.A.;
The A large protein containing zinc finger domains binds to related
T sequence elements in the enhancers of the class I major
T histocompatibility complex and kappa immunoglobulin genes.";
Mol. Cell. Biol. 10:1406-1414(1990).
REMBL; M32019; AAA17534.1; -..
REMBL; M32019; AAA17534.1; -..
REMBL; M52019; AAA17534.1; -..
REMBL; M52019; ZiC2H2.
REMBL; SRO0355; ZiC2H2.
REMBL; SSO0581; ZINC_FINGER_C2H2.1; 2.
REMSCITE; PSSO0581; ZINC_FINGER_C2H2.2; 2.
REMSCITE; PSSO0581; ZINC_FINGER_C2H2.2; 2.
REMSCITE; PSSO157; ZINC_FINGER_C2H2.2; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.3%; Score 35; DB 4; Length 1902; Best Local Similarity 66.7%; Pred. No. 2.4e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1902 AA; 207457 MW; 35BBF0D961E6ED20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    749 AA; 83344 MW; 4DCD10F480EE0257 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1902 AA
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01-NOV-1996 (TrEMBLrel. 01, Last sequenc
01-MAR-2002 (TrEMBLrel. 20, Last annotat
DNA-binding protein (Mbp-1) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00434; TOP4c; 1.
TIGRFAMS; TIGR01062; parC Gneg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.3
Best Local Similarity 77.8
Matches 7; Conservative
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1590 WYPAGLTYS 1598

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MEDLINE=94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
Ine Y.S., Shimizu J., Yoda K., Yamasaki M.;
Ine Y.S., Shimizu J., Yoda K., Yamasaki M.;
Ine S., Sini S., Sani S., Yokoli S., Sani S.,
                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encodes a factor involved in mitochondrial import of yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De naan M., Grivell L.A., Maarse A.C.,
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Mol. Cell. Biol. 13:6442-6451(1993).
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Matches 6; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 72.998 Million cell updates/sec June 4, 2003, 13:04:34; Search time 6.25 Seconds Run on:

1 eevvpxgmsys 11 AUDET-909-1 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 112892 segs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	fusoba	074377 schizosacch	_	Q04351 clostridium	P15822 homo sapien		_	0	-				-	₩.		homo sa	rattus	Q04827 rattus norv		_	Q90459 brachydanio		gallus		-	homo		เลนต	00	4677 haemo	55 homo	ошоч 9	P52384 human herpe
SUMMARIES	ID	ARB	SULH SCHPO	Y11K TYDVA	Y1A9_CLOAB	ZEP1 HUMAN	CY14 NEUCR	A10C HUMAN	RL20 MYCPU	Y990 CAMJE	AROA VIBCH	CC37_SCHPO		BCN5_CLOPE	LTBS HUMAN		LTBL_HUMAN	LTB1_RAT	CGD2 RAT	CGD2 HUMAN		CGD1_BRARE	CGD1 XENLA				CGD3 HUMAN	CGD1 HUMAN		- 1	1			PRTP_HSV6U
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P32784 saccharomyc	Q62671 rattus norv	P28931 tomato aspe	P16916 escherichia	P16918 escherichia	P16917 escherichia	095071 homo sapien	P17280 chimpanzee	Q10676 mycobacteri	O59619 pyrococcus	Q9hnu2 halobacteri	O05756 mycobacteri
SCT1_YEAST	EDD_RAT	V1A_TAV	RHSA ECOLI	RHSC_ECOLI	RHSB_ECOLI	EDD HUMAN	REV SIVCZ	COBH MYCTU	PURQ_PYRHO	PURQ_HALN1	PURQ_MYCLE
Н	<del>,  </del>	-	Н	н	-	-	Н	Н	1	Н	н
759	920	993	1377	1397	1411	2799	124	208	223	224	224
61.5	61.5	61.5	61.5	61.5	61.5	61.5	59.6	59.6	59.6	9.69	59.6
32	32	32	32	32	32	32	31	31	31	31	31
34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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                                             15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annoctation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
                                                                                                      Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
            PRT; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE010554; AAL94625.1; ALT_INIT.
InterPro; IPR005483; CPase_L.
InterPro; IPR005481; CPase_L. D2.
InterPro; IPR005481; CPase_L. D2.
InterPro; IPR005481; CPase_L. D3.
InterPro; IPR005481; CPase_L. D3.
InterPro; IPR004362; MGS like.
Pfam; PP00289; CPSase_L. Chain; 2.
Pfam; PP02187; CPSase_L. D3; 1.
Pfam; PP02187; CPSase_L. D3; 1.
Pfam; PP02187; CPSase_L. D3; 1.
PRINTS; PR00189; MGS; IL.
PRINTS; PR00189; CPSASE.
                                   15-JUN-2002 (Rel. 41, Created)
            STANDARD;
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                              CARB OR FN0422.
           CARB FUSNN
CARB FUSNN
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Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Rajandram M.A., Lyne M., Lyne R., Stewart A., Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., A Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A Horbby T., Howarth S., Huckle B.J., Hunt S., Jagels K., Junes L., Jones M., Leather S., McDald S., McLean J., Androyd S., McLes M., Leather S., McDonald S., McLean J., Androw P., Moule S., Mongell K., Murphy L., Nibbett D., Odell C., Androw P., Moule S., Bearson D., Guell M.A., Rabbinowitsch E., Stelton J., Simmonds M., Squares R., Squares R., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Bertjens I., Vanstreels E., Rieger M., Schaefer M., Mueller S., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Abaga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Abhakovski G.V., Ussery D., Barrell B.G., Nurse P., The Genzuer esquence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                    OLIGOWERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                   MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
               Arginine biosynthesis; ryrimital ATP-binding; Manganese; Complete protecme.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                         .;
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-!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 1058;
Pred. No. 6.2;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                              MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                  ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPBC3H7.02.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last annotati
Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
PROSITE; PS00867; CPSASE 2; 2
                                                                                                                                                                                                                                                                                              1058 AA; 117451
                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                          546
929
1058
546
1058
210
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                                                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SULH SCHPO
074377;
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                               REPEAT
NP_BIND
NP_BIND
                                                                                       DOMAIN
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SIMILARITY)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92188538; PubMed=1546458; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.; The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monococtyledonous plants."; Virology 187:633-642(1992).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS:
-!- SIMILARITY: CONTAINS 1 STAS DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.2%; Score 37; DB 1; Length 877; 77.8%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56995A8493371E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tobacco yellow dwarf virus (strain Australia) (TYDV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL_1993 (Rel. 26, Created)
01-JUL_1993 (Rel. 26, Last sequence update)
01-CTT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
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POTENTIAL.
POTENTIAL.
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InterPro, IPR002645, STAS.
InterPro, IPR001902, Sulfate_transp.
                                                                                                                                                                                                                                      Pfam; PF00916; Sulfate_transp; 1.
Pfam; PF01740; STRAS; 1.
TIGREAMS; TIGRO0815; sulP; 1.
PROSITE; PS01130; SLC26A; 1.
PROSITE; PS50801; STAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96373 MW;
                                                                                                                                                                                                                                                                                                                        Transport; Transmembrane. IRANSMEM 133 153
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es 7; Conserv
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2221
2221
2221
2292
2444
4614
4614
518
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993),
-!- SIMILARITY: BELONGS TO THE FTSK/SPOIIIE FAMILY.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATC: 024 / DSM 792 / VXM B-1787;
MREDIANG=ATC: 024 / DSM 792 / VXM B-1787;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetcbutylicum.";
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 23;
2; Mismatches 2; Indels
                                                                                                                                                      69.2%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.4; 1; Indels ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168968 MW; FF42037A335A9649 CRC64;
                                                                                                 Hypothetical protein.—
SEQUENCE 102 AA; 11179 MW; A40ECFIE0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AE007866, AAK81629.1; -. EMBL. AE007866, AA46379.1; ALT FRAME.
INCEPTO, IPRO02543, FUSK SPOIITE.
Pfam, PF01580; FUSK SPOIITE; 2.
Hypothetical protein; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
or send an email to license@isb-sib.ch)
                                                                  InterPro; IPR002621; Gemini mov. Pfam; PF01708; Gemini mov; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein CAC3709.
                                 EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 60.0%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium acetobutylicum.
                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                             2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                             7 QVVPSGINYS 16
                                                   PIR; A42452; A42452.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium
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                                                                                                                                                                                                                                                                                                                    LT 4
CLOAB
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0; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Biochemistry 31:3907-3917(1992).

Fiochemistry 31:3907-3917(1992).

FINE SPOTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMBEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CW, OR HIV1.

IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MGC. INTERLEUKIN-2 RECEPTOR, AND INTERPERON-BETA GENES. IT MAY ACTIVE SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2010 (Rel. 40, Last annocation update)
Zinc finger protein 40, (Human immunodeficiency virus type I enhancer-binding protein 1) (HIV-EP) (Major histocompatibility complex binding protein 1) (MIV-EP) (Major histocompatibility complex binding protein 1) (MIV-EP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Biochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fan C.M., Maniatis T.; A DNA-binding two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 2087-2142.
MEDLINE=92232684; PubMed=15678844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
-i- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 2113-2142.
MEDLINE=91064333; PubMed=2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K., Gronenborn A.M.;
                                                                                                                                        2717 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINC-FINGER IN-BETWEEN.
-:- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
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                                    1276 EQKIPMGMSY 1285
                                                                                                                                        STANDARD;
1 EEVVPXGMSY 10
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PDB; 3ZNF; 15-JAN-92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T00497; -.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                           HIVEPI OR ZNF40.
                                                                                                                                                                                                                                                                                                        (PRDII-BF1)
                                                                                                                                        HUMAN
                                                                                                                                                           P15822;
                                                                                                                     ZEP1_HUMAN
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30-MAY-2000 (Rel. 39, Created)
15-UTN-2002 (Rel. 41, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Potential phospholipid-transporting ArPase VC
(Aminophospholipid translocase VC).
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                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. POTENTIAL.
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                                                                                                                                                                                 InterPro; IPR001902; Sulfate_transp. Pfam; PF00916; Sulfate_transp; 1. TIGRPAMs; TIGR00815; Sulp; 1. Pransport; Pransmembrane; Glycoprote:
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MEDLINE=21225279; PubMed=11326269;
                                                                                                                                                EMBL; M59167; AAA33615.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 337-1499 FROM N.A.
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                                                                                                                                                               A37956; A37956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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193
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MEDLINE=94188926; PubMed=8140616;

A Sandal N.N., Marcker K.A.;

Sandal N.N., Marcker K.A.;

Sandal N.N., Marcker K.A.;

T "Similarities between a soybean nodulin, Neurospora crassa sulphate

T "rends Blochem. SG1. 19:19-19(1994).

L Trends Blochem. SG1. 19:19-19(1994).

-!- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.

-!- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.

-!- FUNCTION: Highly expressed, but only in cells subject to sulfur cell intitation, and it is turned on by the positive-acting Cys-3 sulfur regulatory protein.

-!- MISCELLANGOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.

-!- SIMILARITY: BELONGS TO THE SICZ6A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE-91129256; PubMed-1825178;
MEDLINE-91129256; PubMed-1825178;
MEDLINE-91129256; PubMed-1825178;
MEDLINE-91129256; PubMed-1825178;
Medleotide sequence, messenger RNA stability, and DNA recognition elements of cys-14, the structural gene for sulfate permease II in
                                                                                               SMART; SMUUJSS; AHE CARE, 1.
PROSITE; PS00028; ZINC FINGER CZH2 1; 4.
PROSITE; PS50121; ALION, ZINC FINGER CZH2 2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; 3D-structure.
DOMAIN 406 428 CZH2-TYPE.
ZINC FINGERS.
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 1; Length 2717; Pred. No. 70;
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                                                                                                                                                                                                                     C2H2-TYPE.
POLY-SER.
C2HC-TYPE (POTENTIAL).
ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Sulfate permease II.
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                                  InterPro; IPR000822; Znf C2H2.
Pfam; PF00096; zf-C2H2; 5.
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                                                                        PRINTS; PR00048; ZINCFINGER.
SMART; SM00355; ZNF_C2H2; 4.
                                                                                             C2H2; 4.
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Best Local Similarity
Matches 6; Conserv
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
Hrrzing L.B.K., Kim S.-J., developerating ATPase gene ATP10C maps adjacent to UBB3A and exhibits similar imprinted expression.";
Am. J. Hum. Genet. 68:1501-1505(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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MEDLINE=98290545; PubMed=9628581;
Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 788;
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"prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5.31-39(1998).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
-!- SIDECELPLUAR LOCATION: Integral membrane protein (By similarity).
-!- TISSUE SPECIFICITY: Wide expression, with highest levels in kidney, followed by lung, brain, prostate, testis, ovary, and small intestine.
-!- DISBASE: Defects in ATP10C may be a cause of Angelman syndrome (AS), also known as 'happy puppet syndrome'.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR001454; Hlgnase/hydrlase.
InterPro; IPR00102; Hydrolase; 1.
PRINTS; PR00119; CAPATPASE.
PROSITE; PS001154; ATPASE_E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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AAK33100.1;
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Multigene family.
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                                                                                                                                                Gaps
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Mycleic Acida Res. 29:2145-2153(2001).
Nucleic Acida Res. 29:2145-2153(2001).
INCTESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL RND IS SUBUNIT, IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS OF THAT SUBUNIT (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.
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MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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 PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                65.4%; Score 34; DB 1; Length 1499; 72.7%; Pred. No. 62;
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Mypulist; MYPU 2610; .

InterPro; IMPO1081; Ribosomal L20.

Pfam; PF00453; Ribosomal L20; I.

PRINTS; PR00062; RIBOSOMALL20; .

ProDom; PD002389; Ribosomal L20; 1.

TIGREAMS; TIGREAMS; TIBOSOMAL L20; 1.

PROSITE; PS00937; RIBOSOMAL L20; 1.

Ribosomal protein; rRNA-binding; Complete proteome.
427 427 PHOSPHORYLATION (BY SIMILARI)
1031 1031 MAGNESIUM (BY SIMILARITY).
1035 1035 MAGNESIUM (BY SIMILARITY).
467 470 POLY-GLU.
318 38 0 -> R (IN REF. 3).
1499 AA, 167687 MW, D4996A4D0635A68D CRC64;
                                                                                                                                                 3; Indels
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15-UNN-2002 (Rel. 41, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L20.
RPLT OR MYPU_2610.
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Matches 8; Conserv
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RESULT

POTENTIAL. CYTOPLASMIC (POTENTIAL).

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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                              Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (BC 2.5.1.19) (5-enclpyruvylshikimate-3-phosphate synthase) (BPSPS synthase)
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NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression and characterization of Campylobacter jejuni
benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%; Score 33; DB 1; Length 253; 55.6%; Pred. No. 16; 2; Indels tive 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein, Complete proteome.
SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;
                Y990_CAMJE STANDARD; PRT; 253 AA. P45489; Q9PNV0; 01-NOV-1995 (Rel. 32, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 116-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype Ol;
MEDLINE=20406833; Pubmed=10952301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 160-253 FROM N.A. STRAINS-AFTC 43431 / TGH 9011; MEDI-INE=9547673; PubMed=7730270; Hani E.K., Chan V.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL139076; CAB73246.1; -. EMBL; Z36940; CAA85392.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 55.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 DIFPSGMSY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMSY 10
                                                                                                                                                                                Campylobacter jejuni
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=NCTC 11168;
                                                                                                                                                                                                                                             NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AROA OR VC1732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                      CJ0990C
Y990 CAMJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AROA_VIBCH
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE-2184401; PubMed=11859360;
MEDLINE-2184401; Rajandream M.A., Lyne M., Lyne R., Stewart A., Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyviny1)-3-phosphoshikimate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
HS90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00275; EPSP syntase; 1.
ProDom; PD001867; EPSP syntase; 1.
ProSITE; PS00104; EPSP SYNTHASE 1; 1.
PROSITE; PS00886; EPSP SYNTHASE 2; 1.
Aromatic amino acid biosynthesis; Transferase; Complete proteome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
                                                                                                                                                                                                                                                                                         "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Westwood P.K., Preston N.C., Fantes P.A., "Schizosaccharomyces pombe cdc37 gene."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR001986; EPSP syntase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004251; AAF94882.1; -.
TIGR; VC1732; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sixth step.
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audet-909-1.rsp

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RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Richerford K., Rutter S., Saunders B., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Steyens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Gabler C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Daga R.R., Cruzado L., Jimene S., Gloux S., Lelaure V., Motier S.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
Ractiviti G.V., Ussery D., Barrell B.G., Nurse P.;
Ractivity (By similarity).
RC --- FUNCTION: With Hsp90 it forms a complex that binds to several kinds to several continuity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.V., Ucki K., Billings R. Ramaswamy S., Mohrenweiser H.W.,
Scheithauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glioma tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Porms a complex with Hsp90. Interacts with a number of kinases (By similarity).
-!- SUBCELLULAR LOCATION: CYCOPISSMIC (By similarity).
-!- SIMILARITY: BELONGS TO THE CDC37 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Q9NZM5; Q9NPP1; Q9NFR4; Q9UFI2; Q9BTC6; Q9HAX6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 466; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ132376; CAB38757.1; -.
EMBL, AL049769; CAB43371.2; -.
Chaperone; Cell division. Cell cycle.
SEQUENCE 466 AA; 52554 NW; 647238B34CABB3C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ132377; CAB38758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 DSAIPGGMSY 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLTSCR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                              R -> Q.

/FTIG=VAR 011486.

GSS -> HEG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEQLWEKLAKÇGELPREVRRAQARLINPSATRAKPGPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVERP -> SGRSSYGRSWPSRASSPGGAQGPSPVAQPFCN
KGPNPAPGHRIAA (IN REF. 3).
SDNPLDRPLVGQDEFFLE -> LNNPDKPVVWPGCLFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IN REF. 3).
A -> S (IN REF. 2; AAH04229).
D -> H (IN REF. 3).
PEGNILRDRFKSFQRRNMIEPRERAKFKRYKVKLVEKRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REIQ -> VLTVSCRCAPCPVMTPSLLPVPPRGYGRHHGCP
WAGPVGPMPRG (IN REF. 5).
EGNILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFR
                                                                                                 SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIQL -> RGQHSFETGSRAFRGGI (IN REF. 7F18923E348CB52B CRC64;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                               Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 63.5%; Score 33; DB Similarity 60.0%; Pred. No. 30; 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC010095; AAH10095.1; -. EMBL; AF296124; AAG30413.1; -. EMBL; AL359335; CAB94786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF182076; AAF62873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC004229; AAH04229.1; -. BC006311; AAH06311.1; -.
                                                                                                                                                                                           Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 AA; 54417 MW;
                                                                                                                                                                                                                                                                         SEQUENCE OF 218-477 FROM N.A.
                                                                                                                                                                                                                     SEQUENCE OF 12-478 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL359336; CAB94787.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-2DPAGE; Q9NZM5; HUMAN
Genew; HGNC:4333; GLTSCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL122063; CAB59242.1;
region.";
Genomics 64:44-50(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.
191
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                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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417
433
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                                                  TISSUE=Muscle;
                                                                                                                                                                                                                                                                                        rissue=Testis;
                                                                                                                                                                                   infection.
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RESULT 14
LTBS_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Garnier T., Cole S.T.;
"Studies of UV-inducible promoters from Clostridium perfringens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens."; Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE=87057020; PubMed=2877971;
Garnier T., Cole S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and molecular genetic analysis of the bacterioring perfection of the bacterioring of the bacterioring perfection perfection of the bacterioring perfection of the bacterioring perfection pe
                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pIP404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96699 MW; F4E5E8971C31C6C6 CRC64;
                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Bacteriocin BCNS.
                                                                                                                                                                                          890 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacteriocin-encoding gene.";
J. Bacteriol. 168:1189-1196(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88336297; PubMed=2901768;
Garnier T., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00287; SH3b; 3. Antibiotic; Bacteriocin; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2:607-614(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR003646; SH3 bac.
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EMBL; M32882; AAA98249.1; -.
PIR; A30481; A30481.
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                                                                                                                                                                                                                                                                                                                                                                                  Clostridium perfringens.
                                                                                                                                                                                          STANDARD;
                                                239 EVAPAGASYN 248
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EVVPGGFTY 178
2 EVVPXGMSYS 11
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P08696;
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MEDLINE=90275601; PubMed-2150783;

MEDLINE=90275601; PubMed-2150783;

Mayazono K., Claesson-Welsh L., Heldin C.-H.;

Myazono K., Claesson-Welsh L., Heldin C.-H.;

TGF-beta 1 binding protein: a component of the large latent complex of TGF-beta 1 with multiple repeat sequences.";

Cell 61:1051-1061(1990)

C. !- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS COMPOSED OF THE TGF-BETA1 MOLECULE NONCOALBENTA ASSOCIATED WITH A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-BETA1-BP TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.

C. !- ALTERNATIVE PRODUCTS: 2 isoforms; a short form (shown here) and a long form (AC Q14766); are paroduced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR00151; Asx_hydroxyl.

BR InterPro; IPR00151; EGF_like.

DR InterPro; IPR001511; EGF_Ca.

DR InterPro; IPR0012812; Fibril-assoc.

BR InterPro; IPR001281; EGF_Ca.

BR Ffam; PP00603; TB; 4.

DR SMART; SM000179; EGF_Like, 4.

DR SWART; SM00010; ASX_HYDROXYL; 13.

PROSITE; PS00010; ASX_HYDROXYL; 13.

PROSITE; PS01187; EGF_Li.

PROSITE; PS01187; EGF_Z; 11.

DR PROSITE; PS01186; EGF_Z; 11.

PROSITE; PS01187; EGF_CA; 15.

W Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal;

Glycoprotein; Alternative splicing.

T SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                  01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Latent transforming growth factor beta binding protein 1S precursor (Transforming growth factor beta-1 binding protein 1) (TGF-betal-BP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LATENT TRANSFORMING GROWTH FACTOR BETA
                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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RGF-LIKE 2, CALCIUM-BINDING
EGF-LIKE 3, CALCIUM-BINDING
EGF-LIKE 4, CALCIUM-BINDING
EGF-LIKE 5, CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING PROTEIN 1S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PIM: The N-terminus is blocked.
-!- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M34057; AAA61160.1; -.
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GlycoSuiteDB; P22064; -.
Genew; HGNC:6714; LTBP1.
STANDARD;
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                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                               PHILIPHELL AND DANKARANA AND DANKARANA DANKARA
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Length 1394;

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EGF-LIKE 15.

CELL ATTACHMENT SITE (POTENTIAL).

BY SINILARITY.

BY SINILARITY
                                                                                               EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL)
                                               EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL)
                                                                                                                REPEAT C.
EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 15.
           (POTENTIAL)
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SEQUENCE

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STRAIN=El Tor Nis961 / Serotype Ol;

MEDLINE=20406833; PubWed=10952301;

MEDLINE=20406833; PubWed=10952301;

Heidelboerg U.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {RNA}(N).
-i. SUBGNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN (By similarity).
-i. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta' chain (BC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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Pred. No. 93;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A2.
Pfam; PF016824; RNA_pol_A2; 1.
Pfam; PF01884; RNA_pol_A2; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
                                                 Indels
                                                 3; Mismatches
               Score 33;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE004121; AAF93502.1; -.
HSSP, Q9KWU6; 1HQM.
TIGR; VC0329; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 63.5%;
Local Similarity 50.0%;
les 5; Conservative
Query Match
Best Local Similarity 45...
5; Conservative
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                                                                                                                            399 KEICPGGMGYT 409
                                                                                                                                                                                                                     STANDARD;
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                                                                                        1 EEVVPXGMSYS 11
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SEQUENCE 1401 AA
                                                                                                                                                                                                                                                                                                                                                  RPOC OR VC0329.
                                                                                                                                                                                                                     RPOC VIBCH
Q9KVZ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                RESULT 15
RPOC_VIBCH
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Search completed: June 4, 2003, 13:11:44 Job time: 7.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 96.134 Million cell updates/sec June 4, 2003, 13:08:49 ; Search time 11 Seconds Run on:

1 eevvpxgmsys 11 AUDET-909-1 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	gt.]	DB	QI	Description
1	38	73.1	3472	7	T31308	
7	37	71.2	840	Ŋ	T39116	probable sulfate p
ო	37	71.2	877	N	T40413	sulfate permease -
4	36		102	~	A42452	V1 protein - tobac
ហ	36	69.2	1498	7	B97355	DNA segregation AT
9	35	•	225	7	S57810	hypothetical prote
7	35	67.3	425	7	T24111	hypothetical prote
80	35	67.3	670	7	S22293	zinc finger protei
9	35	67.3	749	7	H82691	topoisomerase IV s
10	35	67.3	2717		A34203	DNA-binding protei
11	34	65.4	156		S54619	hypothetical prote
12	34	65.4	252		H69491	
13	34	65.4	544		C82900	probable ABC subst
14	33	63.5	94		I40758	hypothetical prote
15	33	63.5	116		E90544	_
16	33	ε.	165		D69493	
17	33	63.5	253		C81374	
18	33	Э.	259		T34536	
19	33	ω.	284		S75817	hypothetical prote
20	33	63.5	298		T47670	
21	33	ω.	368		F72281	hypothetical prote
22	33	ω,	426		D82163	sphoshikima
23	33	ω.	466		36	cdc37 protein - fi
24	33	63.5	653		D82352	iron(III) ABC trar
25	33	ω.	890		A30481	bacteriocin BCN5 -
26	33	ж.	1028		AF3286	ATP-dependent DNA
27	33	63.5	1152	7	704	conserved hypothet
28			1394		562	transforming growt
29	33	63.5	4	7	G82336	

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0; Gaps

71.2%; Score 37; DB 2; Length 840; 77.8%; Pred. No. 21; in Indels ive 1; Mismatches 1; Indels

Query Match 71.2 Best Local Similarity 77.8 Matches 7; Conservative

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hypothetical prote masking protein pr	nypotnetical prote transport protein rho protein	hypothetical prote cyclin D2 - rat	cyclin D2 - rat cyclin D2 - mouse	cyclin D2 - human cyclin D1 - Africa	cyclin D2 - Africa cyclin D2 - chicke	cyclin D1 - zebra cyclin D3 - human	cyclin D1 - human
T04456 A38261	E97333 PQ0616 T01457	B72481 JC4011	158372 A41984	A42822 S57922	S57925 JC4579	S62730 B42822	A38977
000	0 0 0	0 0	0 0	0 0	0 0	0 0	N
1548	84 175 223	279 288	288 289	289 291	291 291	291 292	295
63.5	61.5 61.5 61.5	61.5 61.5	61.5 61.5	61.5	61.5	61.5	61.5
333	0 0 0 0 0 0	32 32	32 32	32 32	32	32	32
30	8 8 8 8 8 4	35 36	37 38	39 40	41 42	43	45

# ALIGNMENTS

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C,Accession: T31308
R,Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
J. Bacteriol. 180, 5003-5009, 1998
A,Fitle: Genomic analysis reveals chromosomal variation in natural populations of the unc
A,Fatus: T31308
A,Accession: T31308
A,Scatus: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-3472-SGCH>
A,Cross-references: EMBL.AF0833072; NID:g3599393; PID:g3599394; PIDN:AAC62699.1
C,Superfamily: Cenarchaeum symbiosum hypothetical 367K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-840 <HUN>
A;Cross-references: EMBL:AL132779; PIDN:CAB60015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A;Experimental source: Etrain 972h-; cosmid c869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Cenarchaeum symbiosum
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T39116
R;Hurt, C; Aves, S; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A;Reference number: Z21829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.1%; Score 38; DB 2; Length 3472; 54.5%; Pred. No. 59; . tive 4; Mismatches 1; Indels
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
Matches 6; Conservative
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Gaps

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A; Cross-references: EMBL: Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
                                                                                                                                                                                                                                                                                                                hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Percy, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zinc finger protein AT-BP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Decies: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: S22231 178656
C;Accession: S22231 1786501, C; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-225 <MIL>
A;Cross-references: EMBL:U20592; NID:g924625; PIDN:AAA80497.1; PID:g924626
C;Superfamily: plant Kunitz-type proteinase inhibitor
               DB 2; Length 1498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%; Score 35; DB 2; Length 225; 54.5%; Pred. No. 13; tive 3; Mismatches 2; Indels
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                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                           hypothetical protein precursor (clone TPP11) - tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1996
                                                              2; Mismatches
               Score 36;
Pred. No. 6
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A;Introns: 23/3; 56/3; 113/3; 257/2
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             69.2%;
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Best Local Similarity 54.5.
Best Local Similarity 54.5.
                                                              6; Conservative
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32 DEVVPNGKTYA 42
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                                                                                                                1 EEVVPXGMSY 10
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A;Accession: T24111
Query Match
Best Local Similarity
Matches 6: Conserve
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Matches 5; Conserv
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A;Gene: CESP:R10D12.10
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DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported] - Clos Cyspecies (lostridium acetobutylicum Cybeces: Clostridium acetobutylicum Cyber: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 CyAccession: B97355

Fynoling, J.; Barteon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Joaly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

AyTitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cloakseence number: A96900; MUDD:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V1 protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                         Sulfate permease - fission yeast (Schizosaccharomyces pombe)
Sipecies: Schizosaccharomyces pombe
Cipacies: Schizosaccharomyces pombe
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
Cibacession: T40413
Ribyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Ribyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
A;Reference number: 221926
A;Reference number: 221926
A;Reference number: 221926
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-877 <LYN>
A;Cross-references: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
C;Genetics:
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A)Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168
A)EXPERIMENTAL source: Clostridium acetobutylicum ATCC824
C;Genatics: A,Gene: CAC3709
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-102 <MOR>
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A; Cross-references: SGD:S0005539
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Best Local Similarity 66.7
Matches 6; Conservative
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2405 VVPAGLTYS 2413
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Hakaby,

CiSpecies: Xylella fastidiosa

Airicesion: H82691

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A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: I58280; MUID:91187610; PMID:1901405
A;Accession: S22293
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-670 <MIT>
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
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NiAlternate names: major histocompatibility complex enhancer-binding protein 1
NiAlternaten names: major histocompatibility complex enhancer-binding protein 1
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C;Accession: A34203; A34779
R;Fan, C.M.; Maniatis, T.
Genes Dev. 4, 29-42, 1990
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                                                                                                                                                                                                                            A;Cross-references: EMBL:X54250; NID:957519; PIDN:CAA38151.1; PID:957520 A;Note: the authors did not translate the codon for residue 1 C;Superfamily: HIV-EP2 enhancer-binding protein C;Keywords: DNA binding; transcription regulation; zinc finger
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Pred. No. 48;
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Best Local Similarity 66.7%;
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A;Title: A DNA-binding protein containing two widely separated zinc finger motifs that re A;Reference number: A34203; MUID:90169514; PMID:2106471
A;Accession: A34203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1_2717 **FANA:
A;Cross-references: EMRL:XE1435; NID:938017; PIDN:CAA35798.1; PID:938018
A;Cross-references: EMRL:XE1444, 1990
A;Title: A large protein containing zinc finger domains binds to related sequence element A;Reference number: A34779; MUID:90205817; PMID:2108316
A;Accession: A34779; MUID:90205817; PMID:2108316
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Status: S01-1072, NY, 1074-1168, X', 1170-1225, 'V', 1227-1434, 'N', 1436-1607, 'I', 1609-165
A;Cross-references: GB:M32019
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
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A;Residues: 1-156 <DEW>
A;Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR013
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A; Residues: 1-156 < DEH>
A; Residues: 1-156 < DEH>
A; Cross-references: EMBL: X87331; NID: 91041652; PIDN: CAA60762.1; PID: 9829123
R; de Haan, M.; Grivell, L.A.; Maarse, A.C.
B; de Haan, to the Protein Sequence Database, July 1996
A; Reference number: S66877
A; Accession: S66879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Saccharomyces cerevisiae
Cibace: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
Cibaces solul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
Cibacesion: S54619, Active III In.A.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Reference number: S54617
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C, Superfamily: hypothetical protein YOR013w
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RESULT 15

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Nature 390, 364-370, 1997
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A,Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A,Reference number: A62250; MUD:98049343; PMID:9389475
A,Accession: H69491
A,Accession: H69491
A,Accession: H69491
A,Fations preliminary; nucleic acid sequence not shown; translation not shown A,Residues: 1-252 <KLE>
A,Residues: 1-252 <KLE>
A,Cross-references: GB.AE000970; GB.AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264866 C;Superfamily: cell division inhibitor minD
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A; Reference number: I40758; MUID: 95247673; PMID: 7730270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Au2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: C82900 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi. A;Reference number: A82870
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S. K.Hani, E. K.; Chan, V.L.

J. Bacteriol. 177, 2396-2402, 1995
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Pred. No. 13;
2; Mismatches 2; Indels
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A;Molecule type: DNA
A;Residues: 1-94 <RES>
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 75.v.
6. Conservative
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Matches 7; Conservative
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81 EVIPAGMS 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: ABCsbp-5; UU359
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: C82900
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: E90544  
C;Accession: E90544  
R;Chambaud, I:; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001  
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                   508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: MYPU 2610
A,Genetic code: SGC3
C,Superfamily: Escherichia coli ribosomal protein L20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June 4, 2003, 13:14:13
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les 7; Conservative
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E90544
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                        June 4, 2003, 13:11:19; Search time 183 Seconds (without alignments) 38.754 Million cell updates/sec
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1: \cgn2 6/ptodata/1/paa/PCTUS COMB.pep:*
2: \cgn2 6/ptodata/1/paa/USOG =COMB.pep:*
3: \cgn2 6/ptodata/1/paa/USOG =COMB.pep:*
4: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
5: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
6: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
7: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
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21: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
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26: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
27: \cgn2 6/ptodata/1/paa/USOB =COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4569144 segs, 644733110 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Description	Sequence 33980, A Sequence 38185, A Sequence 38532, A Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli
SUMMARIES	PCT-USO1-08631-33980 PCT-USO1-08631-36185 PCT-USO1-08631-38532 US-09-408-020-4 I US-10-027-801-4
DB	1 1 1 1 8 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
% Query Match Length DB ID	1022 1022 1022 3472 3472
% Query Match	76.9 76.9 76.9 73.1 73.1
Score	2 4 4 4 0 0 0 4 4 4 0 0 0 0 0 0 0 0 0 0
Result No.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Sequence 4, Appli Sequence 5207, App Sequence 5207, App Sequence 32486, App Sequence 32486, App Sequence 3259, App Sequence 2598, App Sequence 2598, App Sequence 14785, App Sequence 14785, App Sequence 1744, App Sequence 1744, App Sequence 2902, App Sequence 2902, App Sequence 2811, App Sequence 2811, App Sequence 3921, App Sequence 2911, App Sequence 3321, App Sequence 3321, App Sequence 3321, App Sequence 2811, App Sequence 2811, App Sequence 2, Appli Sequence 131, App Sequence 1191, App	<i>P</i> 4 600
4 US-10-029-120-4 4 US-10-034-623-4 7 US-60-177-646-23-4 4 US-10-029-386-3 4 US-10-029-386-3 5 US-09-134-000-3 7 US-60-112-418-2 6 US-10-219-999-5 7 US-60-312-544-9 1 US-09-791-534-9 1 US-09-791-537-9 1 US-09-791-537-9 2 US-60-324-631-2 7 US-60-324-631-2	DCT-US00-00724-73 1 US-09-704-302A-73 1 US-09-704-302A-73 1 US-09-704-302A-73 1 US-09-704-30-70 1 US-09-1682-4 1 US-09-236-290 1 US-09-128-476-438 1 US-09-328-32-788 1 US-09-328-1768-2 1 US-09-328-1768-2 1 US-09-328-1768-2 1 US-09-328-1768-2 1 US-09-328-1768-2 1 US-09-328-1768-2 1 US-09-328-1768-2 1 US-10-096-534-67-2 1 US-10-096-534-67-2 1 US-09-573-318-2
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#### ALIGNMENT

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RESULT 1
PCT-USG13-33980
Sequence 33380, Application PC/TUSG108631
Sequence 33380, Application PC/TUSG108631
GENERAL INPORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYBEPTIDES
FILE REFERENCE: 21272-049
CURRENT FILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NOS: 60736
SOFTWARE: Custom
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 33980
LENGTH: 1022
TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: DOMAIN
COTHER INFORMATION: EMATRIX, accession number BL00028, p-value=8.714e-09, raw score of THER INFORMATION: 16.07
NAME/KEY: DOMAIN
LOCATION: (986)...(1003)
COTHER INFORMATION: 2inc finger, C2H2 type domain identified by PFam, accession
COTHER INFORMATION: 2inc finger, C2H2, type domain identified by PFam, accession
COTHER INFORMATION: 2inc finger, C2H2, E-value=4.2e-28, PFam score of 106.8
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; Sequence 4, Application US/09408020; GENERAL INFORMATION:
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; GENERAL INFORMATION:
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2294 EDVIPRGISFS 2304
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Matches 6; Conservative
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                                               ORGANISM: Homo sapiens
                                                                                          NAME/KEY: DOMAIN
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    LENGTH: 1022
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US-09-408-020-4
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US-10-027-801-4
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OTHER INFORMATION: Zinc finger C2H2 type, domain proteins. domain identified by
OTHER INFORMATION: eMATRIX, accession number BL00028, p-value=8.714e-09, raw score
OTHER INFORMATION: 16.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN
LOCATION: (472)..(1007)
OTHER INFORMATION: Zinc finger, C2H2 type domain identified by PFam, accession
OTHER INFORMATION: name zf-C2H2, E-value=4.2e-28, PFam score of 106.8
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0
                                                                                                        76.9%; Score 40; DB 1; Length 1022; 80.0%; Pred. No. 1e+02; tive 1; Mismatches 1; Indels
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80.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILER REFERENCE: 2127-049
FILER REFERENCE: 2127-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR PELLONG DATE: 2000-03-31
PRIOR PELLONG DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLSECOM
SEQ ID NO 36185
LENGTH: 1022
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
FILLS REPERENCE: 2127-049
CURRENT APPLICATION NUMBER: 90/540,217
FULNG PAPLICATION NUMBER: 09/649,167
PRIOR PAPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 38532
                                                                                                                                                     1; Indels
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                    ; LOCATION: (1).\(\tilde{\text{.}}\).(1022)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-33980
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OTHER INFORMATION: Xaa = X or * as defined in Table 2
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                                                                                 Query Match
Best Local Similarity 80.0%;
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nes 8; Conservative
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64 EVVPPGVSYS 73
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64 EVVPPGVSYS 73
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NAME/KEY: misc_feature
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COCATION: (966)...(1003)

OTHER INFORMATION: Zinc finger C2H2 type, domain proteins. domain identified by OTHER INFORMATION: EMATRIX, accession number BL00028, p-value=8.714e-09, raw score of OTHER INFORMATION: 16.07

NAME/KEY: DOMAIN

LOCATION: (472)...(1007)

OTHER INFORMATION: Zinc finger, C2H2 type domain identified by PFam, accession OTHER INFORMATION: name zf-C2H2, B-value=4.2e-28, PFam score of 106.8

NAME/KEY: misc feature

NAME/KEY: misc feature
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APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
TITLE DEPERBNCE: DCORP.002A
CURRENT FILING DATE: 1999-09-29
EARLIER APPLICATION NUMBER: 60/102,294
EARLIER APPLICATION NUMBER: 60/102,294
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Swanson, Robert A.
APPLICANT: Schleger, Christa
APPLICANT: Schleger, Christa
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.9%; Score 40; DB 1; Length 1022; Best Local Similarity 80.0%; Pred. No. 1e+02; Matches 8; Conservative 1; Mismatches 1; Indels
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LENGTH: 3472
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                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10027806;
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
NUMBER OF SEQ ID NOS: 123
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
IBNGTH: 3472
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GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Rohert A.
THILE OF INVENTION NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
TITLE OF INVENTION NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DOORP.002A
CURRENT FILING DATE: 2001-12-21
FRIOR PELICATION NUMBER: BARLIER APPLICATION NUMBER: 09/408,020
FRICOR FILING DATE: BARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.1%; Score 38; DB 24; Length 3472; 54.5%; Pred. No. 1.1e+03; tive 4; Mismatches 1; Indels (
                                                                                            Score 38; DB 24; Length 3472; Pred. No. 1.1e+03; 4; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
                       TYPE: PRT ORGANISM: Cenarchaeum symbiosum
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; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
                                                                                                  73.1%;
54.5%;
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                                                                               Query Match
Best Local Similarity 54.5.
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
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LENGTH: 3472
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US-10-029-120-4
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TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOMOLES THEREOF
FILE REFERENCE: CLOOMOLES: US/60/196,710
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7166
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6207
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TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000210
CURRENT APPLICATION NUMBER: US/60/177,646
CURRENT FILLING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 4226
NS-10-1034-623-4

1 Sequence 4, Application US/10034623

5 GENERAL INFORMATION:
    APPLICANT: Swanson, Ronald V.
    APPLICANT: Seldman, Robert A.
    APPLICANT: Schleper, Christa
    TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
    FILE REFERENCE: DCORP.002A
    CURRENT APPLICATION NUMBER: US/10/034,623
    CURRENT FILING DATE: 2001-12-21
    PRIOR APPLICATION NUMBER: 09/408,020
    PRIOR APPLICATION NUMBER: 09/102,294
    PRIOR FILING DATE: 1998-09-29
    NUMBER OF SEQ ID NOS: 123
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.1%; Score 38; DB 24; Length 3472; 54.5%; Pred. No. 1.1e+03; tive 4; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 27; Length 129;
Pred..No. 64;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Cenarchaeum symbiosum
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Best Local Similarity 54.5.
E.hes 6; Conservative
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2294 EDVIPRGISFS 2304
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Best Local Similarity 70.0
Matches 7; Conservative
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US-60-196-710-6207
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US-60-196-710-6207
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Gaps
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Chosen, Sounitra S.
APPLICANT: Fahy, Edin D.
APPLICANT: Tango, Bing
APPLICANT: Tango, Bing
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660081.465P2
CURRENT APPLICATION NUMBER: 1202-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2598
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APPLICANT: Fahy, Eoin D.
APPLICANT: Tahny, Bing
APPLICANT: Tahny, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Giben, Gary W.
APPLICANT: Giben, Gary W.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.466F93
CURRENT APPLICATION NUMBER: US/60/412,418
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FORESEQ FOR WINGOWS Version 4.0
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                          Score 36; DB 15; Length 382;
Pred. No. 2.2e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                   Sequence 2598, Application US/60389987; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2598, Application US/60412418; GENERAL INFORMATION:
                               69.2%;
                        Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 70.v
Trans 7; Conservative
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Best Local Similarity 70.0°
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US-60-389-987-2598
                                                                                                                          3 VVPXGMSYS 11
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US-60-412-418-2598
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US-60-389-987-2598
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LENGTH: 401
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OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32486, Application US/10029386
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annowax Sequence Listing Engine vers, 1.1
SEQ ID NO 32486
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TITLE OF INVEXTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVEXTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-.005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
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                                                                                                                                                            69.2%; Score 36; DB 27; Length 140; 70.0%; Pred. No. 70; tive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO AF002994.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3738, Application US/09134000A; GENERAL INFORMATION:
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                                                                                                                                                                                    Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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97 KEVVPTGHSY 106
                                                                                                                                                                                                                                                         1 EEVVPXGMSY 10
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                                                               TYPE: PRT
ORGANISM: HUMAN
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LENGTH: 382
TYPE: PRT
              SEQ ID NO 2588
LENGTH: 140
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Wed Jun 4 16:50:27 2003
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263 KEVVPTGHSY 272

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0; Gaps
RESULT 15
US-10-219-999-58270
; Sequence S8270, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Joshua
; APPLICANT: APPLICANT: ALL, Jingdong
; APPLICANT: Stein, Joshua
; TILLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFREENCE: 38-10 (52726) C.
; CURRENT APPLICATION NUMBER: US/10/219, 999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; SEQ ID NO 58270
; LEWARTH: 160
; TYPE: PRT
; ORGANISM: Zea mays
US-10-219-999-58270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.3%; Score 35; DB 26; Length 160; Best Local Similarity 66.7%; Pred. No. 1.3e+02; Matches 6; Conservative 2; Mismatches 1; Indels
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23 ELLPVGMSY 31
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Search completed: June 4, 2003, 13:27:19 Job time: 185 secs

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Sequence 184, App
Sequence 108, App
Sequence 108, App
Sequence 26, Appl
Sequence 66, Appl
Sequence 53, Appl
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Sequence 4, Appli
Sequence 4, Appli
Sequence 73, Appl
Sequence 43, Appl
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Sequence 1061, Ap
Sequence 4, Appli
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Sequence 108, App
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Sequence 4, Appli
                                                                                       June 4, 2003, 13:13:35; Search time 14.25 Seconds (without alignments) 79.694 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/USO8 NEW FUB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT NEW FUB.pep:*

3: \cgn2_6/ptodata/2/pubpaa/PCT NEW FUB.pep:*

4: \cgn2_6/ptodata/2/pubpaa/USO6 NEW FUB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

6: \cgn2_6/ptodata/2/pubpaa/USO7 NEW FUB.pep:*

7: \cgn2_6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

8: \cgn2_6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

9: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*

10: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*

12: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*

13: \cgn2_6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-925-300-1061
US-09-923-304-4
US-10-101-921-4
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US-10-027-801-4

US-10-101-464A-73

US-10-101-464A-73

US-10-214-766-43

US-09-924-340-108

US-09-924-500A-108

US-09-946-783-1184

US-10-000-986-108

US-10-000-986-108

US-09-947-387-66

US-09-947-387-66

US-09-947-387-65

US-09-947-387-65

US-09-947-387-65

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US-10-024-066-2
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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RESULT 1  US-10-027-806-4  Sequence 4, Application US/10027806  Sequence 4, Application US/10027806  Sequence 4, Application US/10027806  GENERAL INFORMATION:  APPLICANT: Schleper, Christa  APPLICANT: Schleper, Christa  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM  FILE REFERENCE: DCORP. 002A  CURRENT APPLICATION NUMBER: US/10/027,806  CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 05/500  FILE REFERENCE: DORD: 123  SOFTWARE: FASTER FILING DATE: 1999-09-29  NUMBER OF SEQ ID NOS: 123  SOFTWARE: FASTER FILING DATE: 1999-09-29  SOFTWARE: FASTER FILING DATE: 1999-09-29  SOFTWARE: FASTER FASTER F	Ø	10 30 57.7 30 57.7 31 30 57.7 44 30 57.7 57.7 57.7	6 31 59.6 1053 10 US-09-815-242-1316 7 31 59.6 1407 10 US-09-815-242-10439 8 31 59.6 1426 10 US-09-912-020-340 9 57.7 7 9 US-09-909-062-1	2 31 59.6 381 9 US-09-975-139-5 3 31 59.6 702 9 US-10-280-403-2 4 31 59.6 702 10 US-09-907-479-2	8 31 59.6 192 9 US-09-986-480-171 9 31 59.6 198 10 US-09-731-872-334 0 31 59.6 223 9 US-09-738-626-6449 1 59.6 299 10 US-09-815-242-10697	32 61.5 2799 9 US-10-151-736-4 31 59.6 53 9 US-10-092-154-878 31 59.6 53 10 US-09-764-847-878 31 59.6 59 10 US-09-948-080-14 31 59.6 161 9 US-09-738-626-5124 31 59.6 163 9 US-10-117-846-20	2 61.5 691 10 US-09-925-731-2 2 61.5 1377 10 US-09-815-242-10384 2 61.5 2799 9 US-10-151-736-4
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GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/034,623

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RESULT 6
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Hisgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.102022
CURRENT APPLICATION NUMBER: 09/202-03-18
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 09/228,866
PRIOR APPLICATION NUMBER: 09/102,866
PRIOR APPLICATION NUMBER: FCT/USON/00724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10027801
; Bedlication No. US2003054364A1
; Bublication No. US20030554364A1
; GENERAL INFORMATION:
   APPLICANT: Swanson, Rohaft A.
   APPLICANT: Schleper, Christa
   PRIOR FILING DATE: EARLIER EARLIER APPLICATION NUMBER: 09/408,020
   PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
   NUMBER OF SEQ ID NOS: 123
   SOFTWARE: Fast5EQ for Windows Version 3.0
   SEQ ID NO 4
   LENGTH: 3472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.1%; Score 38; DB 9; I
54.5%; Pred. No. 1.2e+02;
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTEEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 73, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                  TYPE: PRT ; ORGANISM: Cenarchaeum symbiosum US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:| |:|:|
2294 EDVIPRGISFS 2304
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Matches 6, Conservative
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2294 EDVIPRGISFS 2304
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US-10-101-464A-73
                                                                                                                                                                                                                            LENGTH: 3472
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CENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HIMAN CDNAS AND PROTEINS AND USES THEREOF
TITLE REFERENCE: 91.US2.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
CURRENT FILING DATE: 2001-08-06
CURRENT FILING DATE: 2001-08-06
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR PELICATION NUMBER: US 60/298,698
PRIOR PELICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 108
ILENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS

FILE REFERENCE: CA1138

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,734

PRIOR APPLICATION NUMBER: US 60/311,734

PRIOR ELING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTI VERSION 3.2
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                                                                                                                                                                                                           Length 947;
                                                                                                                                                                                                                Query Match 65.4%; Score 34; DB 9; 1
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 60.v.
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-214-766-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 EFVIPAGOSY 232
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ORGANISM: Homo sapiens
US-09-924-340-108
                                                                                                                            TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                  686 VMPSGISYS 694
                                                                                                                                                                                                                                                                                                                      3 VVPXGMSYS 11
                                                                                                                                                                             US-10-101-464A-73
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US-10-214-766-43
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LENGTH: 426
                                                                               SEQ ID NO 73
LENGTH: 947
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-746-783-184
                                                                                                                                                                               TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                    63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.5%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 60.0
Conservative 6; Conservative
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US-10-000-489-108
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                              Gaps
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Publication No. US20030044935A1

GENERAL INFORMATION:

MCCOY, John M.

LaVallie, Edward R.

LaVallie, Edward R.

Racie, Lisa A.

Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.

Howes, Steven H.

Fechtel, Kim

TITLE OF INVENTION: ENCRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
  Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 33; DB 9; Length 478; 60.0%; Pred. No. 1.4e+02; ive 1; Mismatches 3; Indels
Query Match 63.5%; Score 33; DB 9; Length 478
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENCODING THEM
                                                                                                                                  US-09-992-600A-108
; Sequence 108, Application US/09992600A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 231
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Best Local Similarity 60.0.
Best Local 6; Conservative
                                                                                 239 EVAPAGASYN 248
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                                                       2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-600A-108
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US-09-746-783-184
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0
COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             Score 33; DB 9; Length 478;
Pred. No. 1.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 9; Length 478;
Pred. No. 1.4e+02;
1; Mismatches 3; Indels
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APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. US20020150885Alel Fluorogenic or Fluorescent Reporter Molecule
TITLE OF INVENTION: No. US20020150885Alel Fluorescence
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION NUMBER: US 60/061,582
PRIOR PELING DATE: 1997-10-10
PRIOR PELING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: US 60/145,746
PRIOR APPLICATION NUMBER: US 90/168,888
PRIOR APPLICATION NUMBER: US 90/168,888
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PALEONIN VUMBER: US 09/168,888
SEQ ID NO 66
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
TITLE OF INVENTION: UVRIBANTS OF ALTERNATIVE SPLICING
FILE REPERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: II.134453
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
RIOR FILING DATE: 2000-03-29
RIOR FILING DATE: 2000-03-29
RIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 53
LENGTH: 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 32; DB 10; Length 254;
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61.5%; Score 32; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.5;
Matches 5; Conservative 3; Mismatches 2; Indels
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OTHER INFORMATION: Xaa = any amino acid, unknown, or other
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; Sequence 53, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
                           Sequence 66, Application US/09947387; Patent No. US20020150885A1; GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-947-387-66
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US-09-820-843A-26

Sequence 26, Application US/09820843A

Publication No. US20030039963A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COUNCIL OF Scientific and Industrial Research
TITLE OF INVENTION:
TITLE OF INVENTION: USEPUL AS ANTI-INFECTIVES
FILE REPRENCE: 063915

CURRENT PLING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin version 3.0

SEQ ID NO 26

LENGTH: 653
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                        Sequence 108, Application US/1000986

Publication No. US20030096247A1

GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
FILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US9.DIV
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PLING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/293,574
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CTHER INFORMATION: iron(III) ABC transporter, permease protein
NAME/KEY: misc_feature
NAME/KEY: misc_feature
1 OTHER INFORMATION: gi|9654609
US-09-820-843A-26
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Pred. No. 1.4e+02;
1; Mismatches 3; Indels
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Best Local Similarity 60.0
Matches 6; Conservative
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SOFTWARE: JPatent
SEQ ID NO 108
LENGTH: 478
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Sequence 4, Application US/10024066
; Patent No. US20020166134A1
; GENREAL INFORMATION;
; APPLICANT: Field, Loren J.
; APPLICANT: Field, Loren J.
; APPLICANT: Field, Loren J.
; APPLICANT: Field, MUNENTION: CARDIOWYCCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
; TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
; FILE REPRENCE: 7037-450
; CURRENT APPLICATION NUMBER: US/10/024,066
; CURRENT PILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: PCT/US00/16827
; PRIOR PILING DATE: 2000-06-19
; RIOR APPLICATION NUMBER: PCT/US00/16827
; RIOR PILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                   APPLICANT: Field, Loren J.
TITLE OF INVENTION: CARDIOWYCOYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2999-66-18
PRIOR PLICATION NUMBER: PCT/US00/16827
PRIOR APPLICATION NUMBER: PCT/US00/16827
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.5%; Score 32; DB 9; Length 289; Best Local Similarity 60.0%; Pred. No. 1.38+02; Matches 6; Conservative 1; Mismatches 3; Indels
Pred. No. 1.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                  ; Sequence 2, Application US/10024066; Patent No. US20020166134A1; GENERAL INFORMATION:
60.08;
  Best Local Similarity 60.0
Matches 6; Conservative
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73 EEVFPLAMNY 82
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                                                                       1 EEVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
US-10-024-066-2
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US-10-024-066-4
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US-10-024-066-2
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Search completed: June 4, 2003, 13:30:38 Job time: 15.25 secs
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Sequence 73, Appl
Sequence 236, App
Sequence 236, App
Sequence 236, App
Patent No. 5177197
Patent No. 5177197
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Sequence 66, Appl
Sequence 23, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
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                                                                                           4, 2003, 13:09:19 , Search time 9.75 Seconds (without alignments) 33.195 Million cell updates/sec
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Sequence 4,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-637-759B-236

US-08-637-759B-236

US-09-211-945-236

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5177197-30

US-09-215-650-66

US-09-357-952-66

US-09-357-952-66

US-09-357-952-66

US-08-168-888-62

US-08-66-694-4

US-08-660-694-4

US-08-660-744-4

US-08-660-741-4

US-08-660-771-21

US-08-460-772-21

PCT-US93-05000-22

US-08-464-517-22

US-08-463-772-22

US-08-463-772-22

US-08-463-772-22

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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Sequence 6, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 8, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	Plant Cells ication of Plant Cell Signalling	Length 947; ; Indels 0; Gaps 0;	.30
291 5 PCT-US93-05000-6 292 2 US-08-464-517-23 292 2 US-08-246-361A-6 292 2 US-08-246-361A-6 292 3 US-08-463-712-3 295 1 US-07-947-120-8 295 1 US-07-947-120-8 295 2 US-08-464-517-19 295 2 US-08-464-517-19 295 2 US-08-464-517-20 295 2 US-08-246-361A-19 295 3 US-08-246-361A-19 295 3 US-08-464-517-20 295 3 US-08-464-517-20 295 3 US-08-464-517-20 295 3 US-08-464-517-20 295 3 US-08-463-772-19	E 44	.4%; Score 34; DB 4; .7%; Pred. No. 1e+02; e 2; Mismatches 1 US/08637759B	DDRESS: trea L. Pabst One Atlantic Center West Peachtree Street a 50 E FORM: Floppy disk Floppy disk Floppy Sisk Floppy isk
28 32 61.5 30 32 61.5 31 32 61.5 32 61.5 33 33 32 61.5 34 32 61.5 36 32 61.5 37 32 61.5 39 32 61.5 39 32 61.5 40 32 61.5 41 32 61.5 42 43 32 61.5 44 32 61.5 45 45 32 61.5	RESULT 1 US-09-228-986-73 ; Sequence 73, Application US/09228986 ; Patent No. 6359198 ; GENERAL INFORMATION: APPLICANT: Strabala, Timothy APPLICANT: Netewenhuizen, Niels TITLE OF INVENTION: and Their Use in the Mod; FILE REFERENCE: 11000/1020 ; CURRENT APPLICATION NUMBER: US/09/228,986 ; CURRENT PILING DATE: 1999-01-12 ; NUMBER OF SEQ ID NOS: 130 ; SOFTWARF FILLING DATE: 1999-01-12 ; NUMBER OF SEQ ID NOS: 130 ; SOFTWARF PILLING DATE: 1999-01-12 ; NUMBER OF SEQ ID NOS: 130 ; SOFTWARF PILLING DATE: 1999-01-12 ; TYPE: PRT ; TYPE: PRT ; ORGANISM: Pinus radiata	Query Match Best Local Similarity 66.74 Bact Local Similarity 66.78 Matches 6; Conservative Qy 3 VVPXGMSYS 11                 Db 686 VMPSGISYS 694 US-08-637-759B-236   Sequence 236, Application US, Sequence 236, Application US, Sequence 11 NFORMATION:   TITLE OF INVENTION:   TITLE OF INVENTION:   MINDED OF SPOITMATON:   MINDED OF SPOITMATON	CONDENCE AND A CONDEN

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-201-945-236
is Sequence 236, Application US/09201945
is Patent No. 6342215
is GENERAL INFORMATION:
i APPLICANT: David William Holden
i TITLE OF INVENTION: Identification of Genes
i NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
is STRRET: 2800 One Atlantic Center
is STRRET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paber, Patrea L.
REGISTRATION NUMBER: 31,284
REPERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
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TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                    amino acid
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Best Local Similarity
Matches 6; Conserva
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STATE: Georgia
COUNTRY: USA
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                                                                                                                                                                             US-08-871-355A-236
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5177197-51
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADER: Patera L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:
MATCHING TOWNER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:
MATCHING TOWNER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 235, Application US/08871355A
Fatent No. 601569
GENERAL INFORMATION:
FAPLICANT: David William Holden
TITLE OF INVENTION:
CORRESPONDENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 1830.99-3450.
                          APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: 31.284
REFERENCE/DOCKET NUMBER: 31.284
REFERENCE/DOCKET NUMBER: 31.284
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORM
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TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
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Best Local Similarity 60.0
Matches 6; Conservative
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NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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HYPOTHETICAL:
US-08-637-759B-236
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APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Chewe, John A.
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Verwe, John A.
TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-TITLE OF INVENTION: Pluorescence Screening Assays for Caspases, Peptidases, Proteases
TITLE OF INVENTION: Other Enzymes and the Use Thereof
FILE REFERRINCE: 1735,0030001
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US 60/093,642
EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Patentin Ver. 2.0
SSQID NO 66
LENGTH: 10
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APPLICANT: Cai, Sui Xiong
APPLICANT: Carana, John A.
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: No. Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Use Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 66, Application US/09521650; Patent No. 6335429; GENBRAL INFORMATION:
                                                                 ; Sequence 66, Application US/09357952 ; Patent No. 6248904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.5%;
50.0%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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                                                                                                                                   GENERAL INFORMATION:
RESULT 8
US-09-357-952-66
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PAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; WERNSTEDI, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENA; HELDIN, CARL-HENRIN, TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH FACTOR-BETAI-BINDING PROTEIN CURRENT APPLICATION DATA;
                           APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
;MERNSTEDT, CHRISTER,HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
;LIA,HELDIN, CARL-HENRIN,
;TITLE OF INVENTIONS:
;HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
;NUMBER OF SEQUENCES: 53
;CURRENT APPLICATION DATA;
;HING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Patent No. 5177197; ANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; HERLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREI, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENA; HELDIN, CARL-HENRIK; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 33; DB 6; Length 1394; 45.5%; Pred. No. 2.6e+02; tive 3; Mismatches 3; Indels
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Pred. No. 63;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 33; DB 6; Length 65; 45.5%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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      Patent No. 5177197
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5177197-51
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5177197-1
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1-7617715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08460694;
Patent No. 5858655;
GENERAL INPORMATION:
APPLICANT: APADICANT: APADICANTES: 8
CORRESPONDENCE ADDRESS: ADDRESSEE: STERNEY SESSLER, GOLDSTEIN & FOX P.I. STREET: 1100 New York Avenue, N.W., Suite 600;
CITY: Washington
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NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPACE 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 23:
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LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: protein
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  CLASSIFICATION: 424
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                                                                                                                                                                                                                                        # PAPLICANT: Weber, Eckard
# APPLICANT: Weber, Eckard
# APPLICANT: Weber, Eckard
# APPLICANT: Cai, Sui Xiong
# TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
# TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
# TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
# TITLE OF INVENTION: Use Thereof
# TITLE OF INVENTION: Use Thereof
# TITLE OF INVENTION: Use Thereof
# TITLE OF INVENTION NUMBER: US 60/061, 582
# CURRENT FILING DATE: 1998-10-09
# EARLIER APPLICATION NUMBER: US 60/061, 582
# EARLIER APPLICATION NUMBER: US 60/061, 582
# NUMBER OF SEQ ID NOS: 142
# NUMBER OF SEQ ID NOS: 142
# SOFTWARE: PatentIn Ver. 2.0
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Receptor-I-Associated Protein Kinase And Methods
For its Use
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  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.5;
  3; Mismatches
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OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Aggarwal et al.

TITLE OF INVENTION: For INSOC

TITLE OF INVENTION: Receptor-I-Assoc

TITLE OF INVENTION: For Its Use

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dr. Benjamin A. Adler

STREE: Texas

COUNTY: HOUSEON

STATE: Texas

COUNTRY: USA

ZIP: 77071
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MEDIUM TYPE: 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/08580988A
Patent No. 5856161
                                                                                                                                                           RESULT 10
US-09-168-888-66
's Equence 66, Application US/09168888
'Patent No. 6342611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 5; Conservative
  5; Conservative
                                              1 EEVVPXGMSY 10
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; Patent No. 6110700
; GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Pradi Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
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Query Match 61.5%; Score 32; DB 2; Length 152; Best Local Similarity 60.0%; Pred. No. 33; Matches 6; Conservative 1; Mismatches 3; Indels
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18-08-460-744-4
18-08-460-744-4
18-08-460-744-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPTITE: IRM PC compatible
COMPTITE: IRM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCONathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/POCKET NUMBER: 35,279
REFERENCE/POCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-2600
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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Best Local Similarity 60.0°
....hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMSY 10
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STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: V
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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GENERAL INFORMATION:
APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PSPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.5%; Score 32; DB 3; Length 152; 60.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
COMPUTER FLOWER FOR WAR-1991
COMPUTER FLOW FOR WAR-1991
                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609,4070000
TELECOMMUNICATION INFORMATION:
TELEFANE: (202) 371-2600
TELEFANE: (202) 371-2600
TELEFAN: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
COUNTRY: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08193977
Patent No. 5625031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: not relevant
MOLECULE TYPE: peptide
-667-7118-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSY 10
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; STRANDEDNESS: single
; MCDPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-193-977-7

Query Match

Glist, Score 32; DB 1; Length 173;

Best Local Similarity 60.0%; Pred. No. 38;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10

Db 55 EEVFLAMNY 64

Search completed: June 4, 2003, 13:14:58
Job time: 9.75 secan
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd. Copyright

OM protein - protein search, using sw model

June 4, 2003, 13:04:09 ; Search time 28.25 Seconds Run on:

(without alignments) 51.885 Million cell updates/sec

AUDET-909-2

1 eevvpxgmhys 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 101002:\* .: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\* : /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1984.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1984.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1985.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1986.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1986.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1987.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1987.DAT:\*/SIDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1988.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1987.DAT:\*/GTDS2/gcgdata/geneseqgp-embl/AA1987.DAT:\*/GTDS2/gcgdata/g | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT: | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT: | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1996.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1997.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: 'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: 15: 117: 118: 120: 220: 23:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Hepatitis C virus									
qı	ABB80523	ABB80527	ABB80558	ABB80560	ABB80537	ABB80541	ABB80546	ABB80550	ABB80554	ABB80555
!	23	23	23	23	23	23	23	23	23	23
% Query Match Length DB	11	11	11	11	11	11	11	11	11	11
% Query Match	96.4	96.4	96.4	96.4	87.5	87.5	85.7	85.7	85.7	85.7
Score	54	54	54	54	49	49	48	48	48	48
Result No.		7	m	4		9	7	ω	60	1.0

/note= "C-terminal amide" /note= "D-form residue"

WO200208251-A2

31-JAN-2002

Modified-site

19-JUL-2001; 2001WO-US23169. 21-JUL-2000; 2000US-220101P.

tis C	itis C vi	itis C	itis C vi	itis C	itie C	itis C	itis C	itis C	itis	itis C v	itis C v	itis																						
53	3053	052	3052	3052	N	22	N	52	55	356	56	92(	ABB80564	95(	95(	92(	92(	53	53	53	53	54	54	54	54	54	54	)54	54	555	55	)55	55	55
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11	11	11	11:	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	ij	11	11	11
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46	46	45	4	4 5	45	4	4,	4	4	4	4	4.5	4	4.5	4	4	4	4	4	4	4	4	4	4	ĕ	κ̈́	ň	ň	ň	ň	S,	κ'n	č	ñ
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## ALIGNMENTS

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
                                                                                                                                             /note= "N-terminal acetyl"
                                                                                                                             Location/Qualifiers
RESULT 1
ABB80523
ID ABB80523 standard; peptide; 11 AA.
                                                   08-OCT-2002 (first entry)
                                                                                                                                                                               Misc-difference
                                                                                                                               Key
Modified-site
                                                                                                                                                      Modified-site
                                                                                                              Synthetic.
                                   ABB80523;
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activity useful for treating disorders associated with hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 residue 7"
                                                                                                                                                                                                                                                                  ABB80558 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 65; 69pp; English.
                               Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169
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                                                                                                                                                                         11; Conservative
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                                                                                                                                                                                             1 EEVVPXGMHYS
                                                                                                                                                                                                             EEVVPXGMHYS
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                                                                                                                                                               Best Local Similarity
                                                                                                                                   11 AA;
           virus protease
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                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                            virucide.
                                                                                                                                                                                                                                                                                     ABB80558
                                                                                                                                                     Query Match
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                              RESULT 3
ABB80558
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                                                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.
                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                 96.4%; Score 54; DB 23; Length 11; 100.0%; Pred. No. 0.00045; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                              Brunck TK;
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                                                                                                            Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                              ABB80527 standard; peptide; 11
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          (CORV-) CORVAS INT INC.
                              Levy OE,
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                                                                                                                                                                                                                                                                         1 EEVVPXGMHYS
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                                                 WPI; 2002-361643/39
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                               11 AA;
                                                                                         virus protease
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                             Lim-wilby M,
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0
                                   hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Norvaly1 carbony1 forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease -
The sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                   96.4%; Score 54; DB 23; Length 11; 100.0%; Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ....
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11 AA;

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1 EEVVPXGMHYS 11
             Sequence
                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha **etoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                            "Norvalyl carbonyl forming keto-amide linkage with residue 7"
virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                             Gaps
                                                                                                                                                                                                                                                                          Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
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                                                                     96.4%; Score 54; DB 23; Length 11; 100.0%; Pred. No. 0.00045; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Oxymethionine"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                         ABB80560 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2001; 2001WO-US23169.
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                                                                                                                                                                                                                                 (first entry)
                                                                                             11; Conservative
                                                                                                                  1 EEVVPXGMHYS 11
                                                                                                                                      EEVVPXGMHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-361643/39.
                                                                          Query Match
Best Local Similarity
                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus protease
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                                                                                                                                                                                                                                                                                                         Synthetic
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                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
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             Score 54; DB 23; Length 11;
Pred. No. 0.00045;
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Pred. No. 0.0043;
96.4%; Scor.
100.0%; Pred. No. v.
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                                                                                                                                                                                                                                                       ABB80537 standard; peptide; 11 AA.
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90.9%;
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Best Local Similarity 90.55,
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                            11; Conservative
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                                                                                                  1 EEVVPXGMHYS 11
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                                                                                                                                        1 EEVVPXGMHYS
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                                      Similarity
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Synthetic.

virucide.

ABB80541;

ABB8054

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibito
Ity useful for treating disorders associated with hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                              'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                         11
/note= "C-terminal amide"
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK;
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                                 (first entry)
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ses 10; Conserv
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                                08-OCT-2002
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   ABB80546;
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                                                                                                                                                                                                                                                                                                                                        /note= "Norvalyl_carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21
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Pred. No. 0.0043;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           'note= "N-terminal acetyl"
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                                                                                      ABB80541 standard; peptide; 11 AA.
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FEVVPXGQHYS 11
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Matches 10; Conserv
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 0.0067;
0; Mismatches 1; Indels
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ABB80546 standard; peptide; 11 AA.

RESULT 7
ABB80546
ID ABB8

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Sequence Query Match Ŋ

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WO200208251-A2
                                                                                                                                                                                                                                                          virus protease
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ABB80555
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                                                             "Norvaly1 carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                    /note= "N-terminal acetyl"
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                                                                                                                             /note= "C-terminal amide"
                                                                                                    'note= "D-form residue"
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             Location/Qualifiers
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nes 10; Conservative
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                                                                /note=
                                                                                                                                                                                                                                                                                      Levy OE,
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                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                  virus protease
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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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Pred. No. 0.0067;
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                                                          /note= "C-terminal amide"
/note= "D-form residue"
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90.9%;
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Claim 17; Page 64; 69pp; English
WPI; 2002-361643/39.
                                                                                                                                               11 AA;
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    residue 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                         Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease -
                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
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90.9%; Pred. No. 0.0067;
tive 0; Mismatches 1; Indels
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/note= "C-terminal amide"
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                                                                        Brunck TK;
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                                                                                                                                              Claim 17; Page 65; 69pp; English.
                   19-JUL-2001; 2001WO-US23169.
                                    21-JUL-2000; 2000US-220101P.
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                                                                        Levy OE,
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                                                     (CORV-) CORVAS INT INC
                                                                                         WPI; 2002-361643/39
                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                            virus protease
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31-JAN-2002
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                Claim 17; Page 64; 69pp; English
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nes 10; Conservative
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            hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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sequence represents a peptide compound of the invention having
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Pred. No. 0.017;
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Best Local Similarity 90.9
Matches 10; Conservative
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/note= "
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Pred. No. 0.026;
0; Mismatches 1; Indels
80.4%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.026;
                           1; Indels
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90.9%;
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                                                                               EEVVPXGMSYS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                         08-OCT-2002
                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                              ABB80522;
  Query Match
                                                                                                                                                                                                                                                                          virucide
                                                                                                                          RESULT 14
                                                                                                                                        ABB8052
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/note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
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                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protesse inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.4%; Score 45; DB 23; Length 11; 90.9%; Pred. No. 0.026; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                      ABB80524 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-361643/39.
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Best Local Similarity
Matches 10; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus protease
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                       08-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                        ABB80524;
                                                                                                                                                                                                                                                                                                                                                                            virucide.
RESULT 15
ABB80524
ID ABB800
XX
AC ABB80
DT 08-OC
XX
XX
XX
HEPAT
XX
HEPAT
XX
HODIF
FT MODIF
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Gaps

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10; Conservative 1 EEVVPXGMHYS 11 1 EEVVPXGMDYS 11

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Search completed: June 4, 2003, 13:11:13 Job time : 29.25 secs

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Page

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:07:09; Search time 22.5 Seconds (without alignments) 100.734 Million cell updates/sec

AUDET-909-2 56 1 eevvpxgmhys 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 Total number of hits satisfying chosen parameters: 671580 seqs, 206047115 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL 21:\*

sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*
sp\_rodent:\*
sp\_rodent:\*
sp\_virus:\*
sp\_virus:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_vertebrate:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Q8rq86 fusobacteri	09x2e2 thermotoga		099ur5 staphylococ	Q46486 corynebacte	Q8ywp1 anabaena sp	Ogavk4 pisum sativ	Q57489 bacteroides	Q9pc35 xylella fas	Q40479 nicotiana t	Q91w50 nicotiana s	Q38317 lactobacill	Q9xvk4 caenorhabdi	Q9sa71 arabidopsis	Q8tz07 methanopyru	027902 methanobact
ID	Q8RG86	Q9X2E2	оэнгна	Q99UR5	Q46486	QSYWP1	Q9AVK4	Q57489	Q9PC35	Q40479	O9LW50	038317	Q9XVK4	Q9SA71	Q8TZ07	027902
DB	16	16	17	16	7	16	10	7		10			Ŋ	10	17	17
% Query Match Length DB	1063	308	322	1057	208	252	819	139	156	233	237	317	425	510	2042	264
% Query Match	67.9	66.1	66.1	66.1	64.3	64.3	64.3	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	60.7
Score	38	37	37	37	36	36	36	35	35	35	35	35	35	35	32	34
Result No.	Н	7	ო	4	ß	ø		80	σ	10	11	12	13	14	15	16

Q9rxn9 deinococcus Q98hu6 rhizobium 1 Q9rw92 deinococcus Q9xam3 streptomyce Q9xam3 streptomyce			099011 prototheca Q96n44 homo sapien Q8xvq7 ralstonia s Q916j1 pseudomonas Q98fx1 rhizobium l	Q9hg99 mortierella Q9kt98 vibrio chol Q9pkh7 chlamydia m O84218 chlamydia t O29966 archaeoglob	Q9wcw0 avian infec Q9Q1C5s arabidopsis Q9QGT4 avian infec Q9GGT3 avian infec Q9GGT1 avian infec
09RXN9 098HU6 09RW92 09XAM3 027679	Q9KBA1 Q16912 Q9Y0Y6 Q9E1X6 Q9YR01	Q8YJ11 Q9VQL7 Q12479 Q9RDC1	099011 Q96N44 Q8XVQ7 Q916J1 Q98FX1	Q9HG99 Q9KT98 Q9PKH7 O84218 O29966	Q9WCW0 Q9T025 Q9QGT4 Q9QGT3 Q9QGT1
16 16 17 17	15 17 17 17	16 16	8 4 1 1 1 6	16 16 17	22222
279 350 355 360	425 495 637 678 748	1028 2438 156 216	257 273 306 367	426 4441 466 534	542 5545 556 558 64
60.7 60.7 60.7 60.7	60.7 60.7 60.7 60.7	60.7 58.9 58.9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
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11 19 20 21 21	22 2 3 2 2 4 3 2 6 4 3 2 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	22 28 30 30	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 8 8 4 4 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

# ALIGNMENTS

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SEQUENCE FROM N.A.

STRAIN=ATCC 25586;

X MEDLINE=21886394; PubMed=11889109;

X MEDLINE=21886394; PubMed=11889109;

X Apatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

XA Battacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

XA Jasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

A Fonstein M., Kyrpides N., Overbeek R.,

RT "Genome sequence and analysis of the oral bacterium Fusobacterium

RT "nocleatum strain ATCC 25586";

RT J. Bacteriol. 184:2005-2018 (2002).

REMBL, ABO10554; AAL94625.1;

CM Ligase; Complete protecome.

KW Ligase; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                                                                         PRT; 1063 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.9
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                    PRELIMINARY;
                                                                                                    QBRGB6
RESULT 1
                                                                                                                    DDT TO DDT TO DD T
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~ RESULT Q9X2E2 audet-909-2.rspt

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1; Mismatches
        Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium xerosis, and
    75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus.
NCBI_TaxID=158878, 158879;
                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                           3 VVPXGMHY 10
                                                                                                                                                                                                             66 VVPDGLHY 73
Best Local Similarity
Matches 6; Conserv
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SEQUENCE 1057 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-MSBB / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
"Evidence for lateral gene transfer between Archaea and Bacteria from
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                         Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
WCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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SEQUENCE 308 AA, 34778 MW, ADE03603E5101A9D CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
Glucose-fructose oxidoreductase related protein.
                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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        308 AA
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                                                                                                                                                                                                             protease activity modulator HFLK
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EMBL, AL445063, CAC11395.1; -.
InterPro, IPR000683, GFO_IDH_MocA.
Pfam; PF01408, GFO_IDH_MocA. 1.
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InterPro; IPR001310; GED.
InterPro; IPR001972; Stomatin.
Pfam; PP01145; Band 7; 1.
SMART; SM03022; GED; 1.
SMART; SM03022; GED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001819; AAD36885.1; -. TIGR; TM1822; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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        PRELIMINARY;
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41 VVPSGIHY 48
                                                                                                                                                                                                                                                                                                  Thermotoga maritima
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SEQUENCE 322 AA;
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2336;
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09HLHB
1D 09HLHB
1D 09HLHB
1D 01-M
1D
        DDT DDT BE SEN B
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SEQUENCE FROM N.A.

SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);

MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito. T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
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Gaps
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   1; Indels
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                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Carbamcyl-phosphate synthase large chain.
PYRAB OR SAV1203 OR SA1046.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00098; CPSASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; UNKNOWN 2.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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Interpro; IPR004562; MSS-like.
Interpro; IPR00169; SHprot acsite.
Pfam; PP00289; CPSase_L_chain; 2.
Pfam; PF02787; CPSase_L_D2; 2.
Pfam; PF02787; CPSase_L_D3; 1.
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1D Q46486
1D Q4
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DT 011
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SCARECROW.
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Q57489;
                                                                          Q9AVK4;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SPECIES-C.striatum; STRAIN-M82B;

MEDLINE-20194806; PubMed=10732668;

Tauch A., Krieft S., Kalinowski J., Puhler A.;

Tauch S., 409-bp R.plasmid pTP10 from the multiresistant clinical isolate Corynebacterium striatum M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human pathogens.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%; Score 36; DB 2; Length 208; 50.0%; Pred. No. 22;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                          Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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DNA Res. 8:205-213(2001).
EMBL, AP003586. BAB77299.1;
Hypothetical protein; Complete proteome.
SEQUENCE 252 AA; 28831 MW; 925572DA5D1CA519 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U21300; AAC95478.1; -.
EMBL; AF024666; AAG03390.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 208 AA; 23012 MW; F1504BE1ECDE85A6 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Alris63.
                                                                                                                                                    SPECIES=C.xerosis; STRAIN=M82B;
MEDLINE=96117603; PubMed=8559800;
Tauch A., Kassing F., Kalinowski J., Puhler A.;
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Best Local Similarity 50.0
Matches 5; Conservative
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235 EMIVPAGLHF 244
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130 DVIPEGKHYA 139
                                                                          NCBI_TaxID=1725, 43770;
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                                                                                                                            SEQUENCE FROM N.A.
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01-MAR-2002
01-MAR-2002
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STRAIN=CV. ALASKA;
MEDLINE=21231727; PubMed=11333309;
Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;
The Molecular Characterization and in situ Expression Pattern of Pea SCARECROW Gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amultiple site-specific DNA-inversion model for the control of Ompiphase and antigenic variation in Dichelobacter nodosus.";
Mol. Microbiol. 17:183-196(1995).
                                                                                                                     Pisum sativum (Garden pea).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
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MEDLINE=96020672; PubMed=7476204;
Moses E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96257263; PubMed=8654969; Billington S.J., Sinistaj M., Cheetham B.F., Ayres A., Moses B.K., Katz M.E., Rood J.I.; Identification of a native Dichelobacter nodosus plasmid and implications for the evolution of the vap regions."; Gene 172:111-116(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA ligase (Fragment).

Bacteroldes nodosus (Dichelobacter nodosus).

Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
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PROSITE; PS00588; FLAGELLA BB_ROD; UNKNOWN 1.
SEQUENCE 819 AA; 90372 Ww; 41B67Bb6DC7ZADFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                     (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 21, Last annotation update)
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EMBL, AB048013; BAB3155.1; -.
InterPro; IPR00144; Flag_bb_rod.
InterPro; IPR005202; GRAS.
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InterPro; IPR001357; BRCT.
Pfam; PR00533; BRCT; 1.
SMART; SM00292; BRCT; 1.
PROSITE; PS50172; BRCT; 1.
                                     (TrEMBLrel. 17,
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PRELIMINARY;
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                                                       01-JUN-2001
01-JUN-2002
                                       01-JUN-2001
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Query Match
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RA MEDLINE-20366717; Pubbed=10910347;
RA Alvastaback;
RA Alvastaback;
RA Alvastaback;
RA Alvastaback;
RA Barros M.H. C., Arrada D., Baba G.S., Baptiest G.S.,
RA Barros M.H. C., Arrada J.E., Babta G.S.,
RA Barros M.H. C., Contan C. Bala G.S.,
RA Colouboc C., Costa M.C.R., Costan N.C.R.,
Costan N.C.R., Costan R.P.,
Colouboc C., Costan F.F., Costan N.C.R.,
Costan N.C.R., Costan N.C.R.,
RA Fada J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Frada J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Madeira A.M.B.N., Madeira H.M.F., Matina J.P.,
Krieger J.E., Kuramae B.E. Laigtet F., Lambais M.R., Laite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matina J.P.,
RA Haques N.V., Martins B.A.L., Martins E.M.F., Matsukuma A.Y.,
Manck C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Noon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Noon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mondi R.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA G. Silve R.B., Roberto P.G., Rodrigues V.C., Gawasaki H.E.,
A Silveira J.F., Silvestri M.C., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A G. Silve A.C.R., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A G. Suza A.D., Terenzi M.F., Truffi D., Taai S.M., Tsuhako M.H.,
A Caso M.A., Zato M.A., Verjovski-Almeida S., Vettore A.L.,
A Mallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Harla A. C., Sardielli R.C., Salveilla fastidiosa.",
A Harla A. C., Sardielli R. C., Salveilla S., Nettore A.L.,
A Mallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Sago M.A., Zatonali S. J., Savasaki H.E.,
A Mallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Harla A., Sardielli S., Salveilla S., Salveilla
                                                                        Gaps
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55.6%; Pred. No. 27;
iive 3; Mismatches 1; Indels
                               Query Match 62.5%; Score 35; DB 2; Length 139; Best Local Similarity 55.6%; Pred. No. 24; Matches 5; Conservative 3; Mismatches 1; Indels
139 AA; 15052 MW; E0E110AA4B7D4708 CRC64;
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Hypothetical protein; Complete proteome.
SEQUENCE 156 AA; 17144 MW; D8358619C6671A5D CRC64;
                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf1950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004014; AAF84752.1; -. InterPro; IPR002545; CheW.
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es 5; Conservative
                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                  3 VVPXGMHYS 11
                                                                                                                       1 EEVVPXGMH 9
                                                                                                                                                                                                                                                                                                                                        Xylella fastidiosa.
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 SEQUENCE
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"Characterization of gene expression of NSERFs, transcription factors of basic PR genes from Nicotiana sylvestris.";
Plant Cell Physiol. 41:817-824 (2000).
EMBL; AB016264; BAA97122.1; -.
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                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Bepmratophyta; Pagematophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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MEDLINE=95276459; PubMed=7756828;
Ohme-Takagi M., Shinshi H.;
"Ethylene-inducible DNA binding proteins that interact with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF PP2; 1.
SMART; SM00380; AP2; 1.
SEQUENCE 237 AA; 26243 MW; 01BC3EEB51E46298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00380; AP2; 1.
SEQUENCE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
                                                                      vi-NVV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) EREBP-2.
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TT-2002 (TrEMBLrel. 21, Last annotation update)
Ethylene-responsive element binding factor.
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                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
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                                                                                                                                                                    Nicotiana tabacum (Common tobacco).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ethylene responsive element.";
Plant Cell 7:173-182(1995).
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PRINTS; PR00367; ETHRSPELEMNT.
PRODOM; PD001423; TF_AP2; 1.
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PRELIMINARY;
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Best Local Similarity
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1 EEVVPXGMHY 10

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RESULT 10

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        Caenorhabditis elegans.
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EEVKPPGIHF 21
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                                          NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93231538; PubMed=8472861;
Fremaux C., De Antoni G., Raya R., Klaenhammer T.;
Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Engel G., Alternam E., Klein J., Henrich B.;

"Structure of a genome region of the Lactobacillus gasseri temperate phage phi adh covering a repressor gene and cognate promoters.";

EMBL, AJ131519; CAB52540.1; -.

InterPro; IPR002053; GH 25.

InterPro; IPR003665; SH3_bac.

Pron; PR01183; Glyco, hydro, 25; 1.

ProDom; PD004620; GH_25; 1.
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                                                                                                                                                                                                                                      MEDIJUE=99384014; PubMed=10452953; Altermann E., Klein J., Henrich B.; Pyrimary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh."; Gene 236:333-346(1999).
                                                                                                                                          Lactobacillus bacteriophage phi adh.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=12417;
                                                                                                                                                                                                                                                                                                                    MEDIINE=95138034; PubMed=7836307;
Henrich B., Binishofer B., Blaesi U.;
"Primary structure and functional analysis of the lysis genes of
Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34703 MW; 9FF2715EE43561C7 CRC64;
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
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(TrEMBLrel. 2
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94 QAVVPKGRHY 103
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SEQUENCE 317 AA; 34
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Gene 126:61-66(1993).
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Matches 6; Conserv
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                                                                                     01-NOV-1996 (
01-NOV-1996 (
01-JUN-2002 (
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Q9XVK4
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Rhabditidae; Peloderinae; Caenorhabditis.
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Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 76; 2; Indels 1ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                          Genome sequence of the nematode C.elegans: A platform for
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                                                                                                                Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                    425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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ProDom; PD000001; Euk pkinase; 1.
PROSTTE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
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                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81109; CAB03241.1;
InterPro; IPR000719; Euk pkinase.
                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916;
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Matches 6; Conservative
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D Q8TZO7 PRELIMINARY; PRT; 2042 AA.

AC Q8TZO7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein of the CobN/Mg-chelatase family.

GN MC0134.

Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC McMLTAXID=2120;
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA SLEARIN-ANJ / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA SLEARIN-ANJ / Shakhova V.V., Belova G.I., Aravind L.,
RA Sherbinina O.V., Shakhova W.N., Wolf Y.I., Stetter K.O.,
RA Malyth A.G., Koonin E.V., Kozyarkin S.A.,
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RT and monophyly of archaeal methanogens.";
RT and monophyly of archaeal methanogens.";
RC Complete protecome.
SQ SEQUENCE 2042 AA; 227716 MW; 83B6E092A62C112A CRC64;

Query Match
Best Local Similarity 75.0%; Pred. No. 4+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Search completed: June 4, 2003, 13:13:25 Job time: 24.5 secs

924 EVVPIGLH 931

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:04:34; Search time 6.25 Seconds (without alignments) 72.998 Million cell updates/sec

AUDET-909-2 Title: Perfect score:

1 eevvpxgmhys 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	escr	interior of the contract of th	staphy	_	P31619	003010	P36148	035586		Q99158 yarrowia li				P13390 bacteriopha	P08858		Q04827		P30280	Q90459 brachydanio	xenopus	gallus	xenopus	gallu	homo s	homo	mus n			P19887 bacillus an	P32784 saccharomyc	074377 schizosacch	Q9kv29 vibrio chol	↤
SUMMARIES		CARB FUSNN	1	CARB_STAAW	Y11K TYDVA	UME1 YEAST	YK47 YEAST	IDI1 MESAU	GAAB METTH	SLS1 YARLI	PHSL_DESBA	MUTL_BACSU	KPBA CAEEL	VLTF BPT5	TKNK BOVIN	RR2 CHLVU	CGDZ RAT	CGD2 HUMAN	CGD2 MOUSE	CGD1 BRARE	CGD1 XENLA	CGD2_CHICK	CGD2 XENLA	CGD1_CHICK	CGD3_HUMAN	CGD1_HUMAN	CGD1 MOUSE	CGD1 RAT	HYPE AZOVI		SCT1 YEAST		RPOC VIBCH	ZEP1_HUMAN
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P20273 homo sapien P17280 chimpanzee	P97885 rattus norv Q58349 methanococc	P10941 cryphonectr	P52210 ovis aries	P44640 haemophilus	075355 homo sapien	P40739 bacillus su	P27989 moorella th	049230 brassica ol
CD22 HUMAN REV SIVCZ	SZOS RAT Y939 METJA	YHA1 CRYPA	ALFB SHEEP	Y325_HAEIN	ENP3_HUMAN	PTBA BACSU	DCMB MOOTH	ETR1_BRAOL
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# ALIGNMENTS

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
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-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP phosphate + L-glutamate + carbamoyl phosphate.

-!- COFACTOR: Binds three manganese ions (By similarity).
-!- PATHWAY: Arginine blosynthesis, first step.
-!- PATHWAY: Pyrimidine blosynthesis, first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NLSO, / ATCC 700699, and N315;
RUFAIN=NLSO / ATCC 700699, and N315;
RUFORD M., Obte T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RUFORD M., Obte T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RUFORD M., Obte T., Uchiyama I., Ragai Y., Lian J.-O., Ito T.,
Ranamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutahi-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Ranehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba J
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                         OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                   ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
                                            ATP-binding; Manganese; Complete proteome.

OMAIN

A01

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                       Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 1; Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                1058 AA; 117451 MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                     ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1057 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity). SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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  PS00867; CPSASE 2; 2
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190 EIVPNGLNYS 199
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PROSITE;
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-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- SUBJUAT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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-!- CAPALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
-!- CAPALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
-!- COFACTOR: Binds three manganese ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDIINE=22040717; PubMed=12044378;
MEDIINE=22040717; PubMed=12044378;
MEDIINE=22040717; PubMed=12044378;
Nagai Y., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                        OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
MANGANESE I (BY SIMILARITY).
MANGANESE I AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                  PRINTS; PR00098; CPSASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2, 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 1057; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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Bacteria, Firmicutes, Bacillales, Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Manganese; Complete proteome.
                                                          InterPro; IPR005483; CPase L. InterPro; IPR005479; CPase L. D2. InterPro; IPR005480; CPase L. D3. InterPro; IPR005481; CPase L. D3. InterPro; IPR005481; CPase L. N. Prop. PR005481; CPase L. Chain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117171 MW;
                                                                                                                                                                                     Pfam; PF00289; CPSase_L_Chain;
Pfam; PF02786; CPSase_L_D2; 2.
Pfam; PF02787; CPSase_L_D3; 1.
Pfam; PF02142; MGS; 1.
EMBL; AP003361; BAB57365.1; -. EMBL; AP003132; BAB42298.1; -.
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60.0%;
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les 6; Conservative
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                                            P00968; 1CSO.
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P58940;
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102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;

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SO SEQUENCE
                        Query Match
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                  OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                        EMBL; AP004825; BAB94951.1; -.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese.
                                                                                                                                                                                                                                                                           52 ATP (POTENTIAL).
84 MANGANESE 1 (BY SIMILARITY).
89 MANGANESE 1 AND 2 (BY SIMILARITY).
80 MANGANESE 2 (BY SIMILARITY).
80 MANGANESE 3 (BY SIMILARITY).
81 MANGANESE 3 (BY SIMILARITY).
81 MANGANESE 3 (BY SIMILARITY).
81 MANGANESE 3 (BY SIMILARITY).
82 MANGANESE 3 (BY SIMILARITY).
83 MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                       CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                              66.1%; Score 37; DB 1; Length 1057; 60.0%; Pred. No. 16; 2; Indels 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco yellow dwarf virus (strain Australia) (TYDV). Viruses; ssDNA viruses; Geminiviridae; Mastrevirus. NCBI_TaxID=31599;
                                                                                                                                                                                                                                                              ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
 -!- SIMILARITY: BELONGS TO THE CARB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92188538; PubMed=1546458;
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InterPro; IPROD2621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
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1057 AA;
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Matches 6; Conserv
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P31619;
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RECUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=S288C / AB972;

RA

MEDLINE=97131271; PubMed=9169875;

RA Araujo R., Aparicio A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Araujo R., Churcher C.M., Coster F., Davis K., Davis R.W., Cherry J.M., A Dietrich F.S., Delius H., Diraclo T., Dubois E., Duesterhoeft A., Dietrich F.S., Delius H., Diraclo T., Dubois E., Duesterhoeft A., A Hull J., Hebling U., Heumann K., Hilbert H., Hillier L., R.A. Hull S., Hyman R., Johnston M., Kalman S., Keine K., A Municke-Smith S., Howes H.-W., Mirtipati S., Moestl D., RA Municke-Smith S., Namath A., Nettwich U., Oefner P., Pearson D., RA Marller-Auer S., Namath A., Nettwich U., Oefner P., Pearson D., RA Scheren B., Schramm S., Schroeder M., Scharfe M., Schraff M., Schrome B., Schramm S., Schroeder M., Schaff M., Scharf M., Zollner M., Ushinsky S., Vierendeels F., Visser S., Visser S., Namath S., Wallshayk S., Vierendeels F., Wisser S., Namath R., Mallshayk S., Vierendeels F., Wisser S., Namath R., Mallshayk S., Vierendeels F., Wisser S., Namath S., Schroeder M., Schaff M., Schlarf M., Schlarf M., Schlarf M., Schlarf M., Scharf M., Schlarf M., Schlar M., Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                            Gaps
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                                                                                            ö
Score 36; DB 1; Length 102;
Pred. No. 2.3;
                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A364A;
Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
UNEL YEAST
AC Q03010; P87330;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-NOV-1997 (Rel. 35, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Melosis megative regulator UNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD; S0006060; UME1.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
SMART; SM00320; WD40; 3.
PROSITE; PS00678; WD REPEATS_1; FALSE_NEG.
PROSITE; PS50082; WD_REPEATS_2; FALSE_NEG.
                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMEI OR WIMS OR YPLISSC OR LPI7C.
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64.3%;
                                  Best Local Similarity 60.0
Matches 6, Conservative
                                                                                                                                                                                         2 EVVPXGMHYS 11
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7 QVVPSGINYS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=4932;
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SEQUENCE FROM N.A.
                                                                                 Mesocricetus
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                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                van Vliet-Redijk J.C., Planta R.J.;
submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
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01-UUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCPI-METI intergenic region.
                                                                                                     64.3%; Score 36; DB 1; Length 460; 62.5%; Pred. No. 11; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 743;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                               411 451 WD 4.
460 AA; 51022 MW; AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 AA; 83644 MW; 84B9946E56B82F15 CRC64;
               Transcription regulation; Meiosis; Repeat; WD repeat.
PROSITE; PS50294; WD_REPEATS_REGION; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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InterPro; IPR002123; Acyltransferase.
Hypothetical protein; Transmembrane.
                                      WD 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.3%;
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                                                                                                                   Local Similarity 62.5
les 5; Conservative
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85
524
555
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                                                                                                                                                        3 VVPXGMHY 10
                                                                                                                                                                                   85 IVPLGLHY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 VVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                     339
                                                                                                                                                                                                                      RESULT 6
YK47 YEAST
AC P36148;
DT D1-UN-1994
DT 01-UN-1994
DE BACCHAROMYCEE
OC BACCHAROMYCEE
OC SACCHAROMYCEE
OC SACCHAROMYCEE
OC SACCHAROMYCEE
OC SACHAROMYCEE
OC SACHAROMYCEE
OC SACHAROMEM
CC This SWISS-HE
CC C C SEND AND TH
SWISS-HE
DR SACHAROMEM
FT TRANSMEM
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035586;
                                                                            SEQUENCE
                                                                                                       Query Match
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                                       REPEAT
                                                    REPEAT
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ID IDII ME
AC 035586,
DT 30-MAY
DT 30-MAY
                                                               REPEAT
                          REPEAT
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STTTTS
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97373600; PubMed=9228075;
Paton VG., Shackelford J.E., Krisans S.K.;
Paton VG., Shackelford J.E., Krisans S.K.;
Cloning and subcellular localization of hamster and rat isopentenyl diphosphate isomerase. A PTS1 motif targets the enzyme to peroxisomes.";
Le enzyme to peroxisomes.";
J. Biol. Chem. 272:18945-18950(1997).
-!- FUNCTION: CATALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE HOWGALLYLIC SUBSTANTE ISOPENTENYL. (TPP) TO ITS HIGHLY ELECTROPHILIC ALLYLIC ISOMER, DIMETHYLALLYL DIPHOSPHATE (DMAPP).
-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
sopentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                         Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWAY: ISOPRENOID BIOSYNTHETIC PATHWAY WHOSE END PRODUCTS INCLUDE DOLICHOLS, UITAMINS A, D, E, AND K, STEROID HORMONES, CAROTENOIDS BILE ACIDS AND CHOLESTEROL.
-i- SUBCELLULAR LOCATION: Percoxisomal.
-i- SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE I FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0TDN-2002 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales;
Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD004109; IPP isomerase; 1.
Isomerase; Isoprene blosynthesis; Cholesterol biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%; Score 35; DB 1; Length 227; 70.0%; Pred. No. 8.5; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMÍLARITY.
BY SIMILARITY.
MICROBODY TARGETING SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 148 BY SIMILARITY.
225 227 MICROBODY TARGETING SIGNAL
227 AA; 26317 MW; P500A6586385E803 CRC64;
                                    (Isopentenyl pyrophosphate isomerase 1) (IPPI1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 AA.
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ACT SITE 86 86 BY SIMILARITY.
ACT_SITE 148 148 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF003836; AAC53283.1; -
InterPro; IPR002667; IPP isomerase.
InterPro; IPR000086; NUDIX hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHSL DES
P13065;
                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    PHSL DESBA
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libs.chb.ch).
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                        Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Haong L., Kaegle P., Lumm W., Pothier B., Qùu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum T deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).

-!- CATALYIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine + H(2)O = AMP + diphosphate + GMP + L-glutamate.

-!- PATHWAY: GMP biosynchesis.

-!- SIBINAT: HETERODIMER COMPOSED OF A GLUTAMINE AMIDOTRANSFERASE SUBUNIT (A) AND A GMP SYNTHASE SUBUNIT (B) (POTENITAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boisrame A., Beckerich J.-M., Gaillardin C.;
"Slaip, an endoplasmic reticulum component, is involved in the
protein translocation process in the yeast Yarrowia lipolytica.";
J. Biol. Chem. 271:11668-11675 (1996).
-!- FUNCTION: INVOLVED IN THE PROTEIN TRANSLOCATION PROCESS. MAY
INTERACT DIRECTLY WITH TRANSLOCATING POLYPEPTIDES TO FACILITATE
THEIR TRANSPER AND/OR HELP THEIR FOLDING IN THE ER. IT IS NOT
REQUIRED FOR VIABILITY BUT IS ESSENTIAL FOR OPTIMAL GROWTH AT
ELEVATED TEMPERATURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Dipodascaceae, Yarrowia.
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0
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Pfam; PF00958; GMP synt_C, 1.
TIGRFAMs; TIGR00884; guaA_Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62,5%; Score 35; DB 1; Length 308; 63.6%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMP-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP BIND 29 35 ATP (BY SIMILARITY).
SEQUENCE 308 AA; 34403 MW; F2DCF6ED202CAEC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yarrowia lipolytica (Candida lipolytica).
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000850; AAB85215.1; ALT_INIT.
HSSP; P04079; 1GPM.
               MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 20460 / W29;
MEDLINE=96216076; Pubmed=8662639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 EEVVESGLHES 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLS1 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLS1 YARLI
Q99158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
SLS1_YARLI
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01-JNN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (EC 1.18.99.1) (NiFeSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Periplasmic.
-i- MISCELLANEOUS: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS TANANSPORT VEHICLE FOR BOTH SUBUNITS.
-i- SIMILARITY: BELONGS TO THE [NIFE] / [NIFESE] HYDROGENASE LARGE SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The crystal structure of a reduced [NiFeSe] hydrogenase provides an image of the activated catalytic center.";

Structure 7:557-566(1999).
-!- CATALYTIC ACTIVITY: 2 reduced ferredoxin + 2 H(+) = 2 oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREVENT SECRETION FROM ER (POTENTIAL). OACD7EF17540B8E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=88058744, PubMed=3316183; MEDLINE=88058744, Peck H.D. Jr., le Gall J., Przybyla A.E.; Menon N.K., Peck H.D. Jr., le Gall J., Przybyla A.E.; alloning and sequencing of the genes encoding the large and small subunits of the periplasmic (NIFeSe) hydrogenase of Desulfovibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydrogenlyase large chain).
Desulfovibrio baculatus (Desulfomicrobium baculatus).
Bacteria; Proteobacteria; delta subdivision; Desulfomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garcin E., Vernede X., Hatchikian E.C., Volbeda A., Frey M.,
Fontecilla-Camps J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 26; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ferredoxin + H(2).
-!- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Menon N.K., Pect H.D. Jr., le Gall J., Przybyla A.B.
J. Bacteriol. 170:4429-4429(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLS1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
MEDLINE=99306038; Pubmed=10378275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

    J. Bacteriol. 169:5401-5407(1987).

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PROSTIE; PS0014; ER TARGET; 1.
Endoplasmic reticulum; Signal
SIGNAL i 17 POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 AA; 47201 MW;
                                                                                                                                                                                                                                                                                                                EMBL; Z50154; CAA90516.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=899;
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            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A Zevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Ringspi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Joris B., Karamata D., Kasahara Y., Klasch J., Harwood C.R., Henaut A.,
Joris B., Karamata D., Kasahara Y., Klasch J., Kumano M.,
Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96349107; PubMed=8760914;
Ginetti F., Perego M., Albertini A.M., Galizzi A.;
"Bacillus subtllis muts muth operon: identification, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                     PDB; 1CC1; 01-JUN-99.
InterPro; 1PR001501; Ni_hdL.
PEfam; PF001374; NIFSGE Hases; 1.
PROSITE; PS00507; NI_HGENASE_L_1; 1.
PROSITE; PS00508; NI_HGENASE_L_2; 1.
Oxidoreductase; Periplasmic; Nickel; Selenium; Selenocysteine;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1; Length 513;
Pred. No. 50;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                      56683 MW; AC8285A6F80576FC CRC64;
                                                                                                                                                                                                                                             IRON 2.
NICKEL.
IRON 1 AND NICKEL.
IRON 2.
NICKEL.
                                                                                                                                                                                                                                                                                                                          IRON 1 AND NICKEL IRON 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiology 142:2021-2029(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA mismatch repair protein mutl
                                                                                       EMBL; M18271; AAA23375.2; -. PIR; A33101; HQDVLB.
                                                                                                                                                                                                                                                                                                                                                                                                   h 58.9%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                               297 PGGLHYS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                        513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTL BACSU
P49850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168;
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METAL
METAL
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SEQUENCE
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MUTL_BACSU
                                                                                                                                                                                                                                                                             METAL
METAL
METAL
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parto V., Pohl T.M., Portetelle D., Porwollik S., Prescort A.M.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleder R., Scoffone F.,
Asto T., Scanlan E., Schleder R., Scoffone F.,
A Sckiguchi J., Sekowska A., Serox S.J., Serror P., Shin B.S., Soldo B.,
Sckiguchi J., Parkoshi M., Tanaka T., Takahashi H., Takemaru K.,
A Tosato V. Uchiyama S., Vandahol M., Vannier F., Vassarotti A.,
Winters P., Wipat A., Yamanoto H., Wamier F., Vassarotti A.,
Winters P., Wipat A., Yamanoto H., Yamane K., Yasamoto K., Yata K.,
A voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
subtilis."
                                                                                                                                                                                                                                                                                                            NATURE 390; 249-256 (1997).

-I FUNCTION: THIS REPOTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN LEGALS.

-I FUNCTION: THIS REQUIRED FOR DAM-DEPENDENT METHYL-DIRECTED DNA MISMATCH REPAIR. MAY ACT AS A "WOLECULAR MATCHMAKER", A PROTEIN THAT REPAIR. MAY HE FORMATION OF A STABLE COMPLEX BETWEST TWO OR MORE DNA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF BING PART OF A FINAL EFFECTOR COMPLEX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-TEB-1994 (Rel. 28, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Probable phosphorylase B kinase alpha regulatory chain (Phosphorylase kinase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Merazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00058; DNA MISMATCH_REPAIR_1; 1. DNA repair; Complete Proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U27343; AAB19236.1; --
EMBL, Z99112; CAB13578.1; --
HSSP, P23367; 1BKN.
Subrilist, BG11402; mutl.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; NNA mis_repair.
InterPro; IPR004359; HIS_KIN_sig.
Pfam; PF01119; DNA mis_repair.
Pfam; PF02119; AATPase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO0585; mutl; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 EMIVPLTFHYS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAEEL
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KPBA_CAEEL
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Matches
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          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Somith M., Sounders D., Shownken R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterston B., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
Submitted (COT-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PHOSPHORYLAE B KINASE CATALYZES THE PHOSPHORYLATION OF SERINE IN CERTAIN SUBSTRATES, INCLUDING TROPONIN I. THE ALPHA CHAIN MAY BIND CALMODULIN (BY SIMILARITY).
-!- PATHWAY: Glycogen metabolism.
-!- SIMILARITY: BELONGS TO THE PHOSPHORYLASE B KINASE REGULATORY CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage T5.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Glycogen metabolism; Calmodulin-binding.
SEQUENCE 1188 AA; 135558 WW; DE9BB875F3603863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide sequence of the bacteriophage T5 ltf gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 1; Length 1188;
Pred. No. 1.2e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaliman A.V.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLTF BPT5 STANDARD; PRT; 1396 AA. P1330; 048502; 01-JAN-1990 (Rel. 13, Created) 01-FBN-1996 (Rel. 33, Last sequence update) 01-MAY-2000 (Rel. 39, Last annotation update) L-shaped tail fiber protein (LTF protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95309401; PubMed=7789514;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L15188; AAA27954.2; -. PIR; S44754; S44754. WormPep; C14B9.8; CE26870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lett. 366:46-48(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T5-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kryukov V.M.;
                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
                                                                                                                                                                                                                                                                                                                 elegans.
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FEBS
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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-!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGGGGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                            between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-!- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE POLYMANNOSE O ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                     MEDLINE-88289370; PubMed=3267228;
Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nucleotide sequence of bacteriophage T5 DNA at the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 1396;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 986 V -> A (IN REF. 2).
1396 AA; 147989 MW; 18CD2192F65FFFC1 CRC64;
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-!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1988 (Rel. 09, Created)
10-NOV-1988 (Rel. 09, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 126 AA.
[3] PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, M14351; AAA30723.1; -.
EMBL, M1444; AAA30723.1; JOINED.
EMBL, M14449; AAA30723.1; JOINED.
EMBL; M14349; AAA30723.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ001191; CAA04591.1; -. PIR; S01982; S01982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X69460; CAA49220.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAC3 OR NKNB
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P08858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S., Tsudzuki T., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T., Inamura A., Yoshinaga K., Sugiura M.; Hanzina M.; Hamada A., Ohta T., "Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: the existence of genes possibly involved in Chloroplast division."; Proc. Natl. Acad. Sci. U.S., 94:5967-5972 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                     1 20 POTENTIAL.
21 83 NEUROKININ B.
86 95 126 AMIDATION (G-96 PROVIDE AMIDE GROUP).
95 95 AMIDATION (G-96 PROVIDE AMIDE GROUP).
126 AA; 13871 MW; 446EFF433498ECG59 CRC64;
                                                         Probom, PD020370; Neurokinin; 1.
PROSITE, PS00267; TACHYKININ; 1.
Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%; Score 32; DB 1; Length 267; llarity 40.0%; Pred. No. 40; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                          57.1%; Score 32; DB 1; Length 126; 66.7%; Pred. No. 19; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribosomal protein, Chloroplast.
SEQUENCE 267 AA; 30699 MW; 7903075340BD900F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Chloroplast 30S ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AB001684, BAA57862.1; -.
InterPro; IPR001865; Ribosomal S2.
Pfam; PR001318; Ribosomal S2, 1.
PRINTS, PR00395; RIBOSOMĀLS2.
TIGRFAMS; TIGR01011; rpsB bact; 1.
PROSITE; PS00962; RIBOSOMĀL S2_1; FALSE NEG.
PROSITE; PS00963; RIBOSOMĀL S2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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STRAIN=IAM C-27 / Tamiya;
MEDLINE=97303241; PubMed=9159184;
EMBL; M14350; AAA30723.1; JOINED.
                  PIR; A25905; A25905.
InterPro; IPR003635; Neurokinin.
InterPro; IPR002040; Tachykinin.
                                                                                                                                                                                                                                                                            Local Similarity 66.7
les 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMH 9
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Matches 4; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlorella vulgaris.
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P56351;
                                                                                                                                                                                                         MOD RES
SEQUENCE
                                                                                                                                                                                                                                                              Query Match
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Gaps

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Search completed: June 4, 2003, 13:11:45
1 EEVVPXGMHY 10
                 EDMIQSGMHF 17
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:08:49; Search time 11 Seconds (without alignments) 96.134 Million cell updates/sec

1 eevvpxgmhys 11 AUDET-909-2 56 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	ftsH proteinase ac	carbamoy1-phosphat	V1 protein - tobac	hypothetical prote			ρμ	DNA binding protei	GMP synthetase, su	hypothetical prote	TSI8.1 protein - A	diphthine synthase	hypothetical prote	3-dehydroguinate s	probable DNA ligas	cell division prot	щ		hypothetical prote	ATP-dependent DNA	hypothetical prote	polyamine transpor	conserved hypothet	probable amino aci	amino acid antipor	finger protein (cl	cytochrome-c3 hydr	0	0.000 Con 1.00 To 1.00
SUMM	DI	A72207	F89892	A42452	AE2001	S69046	538143	D82618	T02590	H69194	T24111	G86430	G69117	C75538	B75478	T35025	E69086	C83903	858132	T28717	AF3286	<b>S54619</b>	E83607	G82253	G71542	H81697	865811	HODVLB	A69284	TOBECA
	DB	1 01	~	7	7	0	~	7	7	~	N	7	~	N	~	7	7	~	~	N	~	N	7	a	~	~	7	-	N	c
	Length	308	1057	102	252	460	743	156	233	311	425	510	264	279	350	355	360	425	426	495	1028	156	367	441	466	466	487	514	534	272
do (	Query	66.1	66.1	64.3		64.3	64.3	62.5	62.5	62.5	62.5	62.5	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	58.9	58.9	58.9	58.9	58.9	58.9	58.9	58.9	0
	Score	37	37	36	36	36	36	35	35	35	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	23
í	Result No.	н	a	ю	4	ιΩ	9	7	80	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	000

DNA mismatch repai	macrophage-stimula	C14B9.8 protein -	L-shaped tail fibe	hypothetical 367K	tachykinin B precu	heme exporter prot	hypothetical prote	ribosomal protein	ribosomal protein	probable ThuA prot	hypothetical prote	cyclin D2 - rat	cyclin D2 - rat	cyclin D2 - mouse	cyclin D2 - human
A69663	JC5061	S44754	836851	T31308	A25905	D71640	S57810	E97120	T07215	C95881	T25737	JC4011	158372	A41984	A42822
7	Н	N	N	N	N	~	N	7	N	7	~	~	7	7	N
627	716	1257	1396	3472	126	197	225	233	267	270	283	288	288	289	289
58.9	58.9	58.9	58.9	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

-	
RESULT 1	A72207

ftsH proteinase activity modulator HflK - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C;Accession: A72207 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Nature 399; 323-129, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seqn
A;Acteference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72207
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <ARN>
A;Residues: 1-308 <ARN>
A;Coss-references: GB:AE001819; GB:AE000512; NID:g4982396; PIDN:AAD36885.1; PID:g4982404
A;Experimental source: strain MSB8
C;Genetics: TM1822
C;Superfamily: erythrocyte band 7 integral membrane protein

Gaps ; 0 Query Match 66.1%; Score 37; DB 2; Length 308; Best Local Similarity 75.0%; Pred. No. 10; Matches 6; Conservative 1; Mismatches 1; Indels

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3 VVPXGMHY 10 ||| |:|| 41 VVPSGIHY 48 g ð

#### RESULT 2

carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001 C;Accession: F89892

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A; Accession: F89892

A; Status: preliminary A; Molecule type: DNA

A;Residues: 1-1057 <KUR> A;Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149 A;Experimental source: strain N315

C; Genetics:

A;Gene: pyrAB C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin (

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Gaps

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-156 <SIM>A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
B;Simpson, A.J.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A.Briones, M.R.S.; Bunco, M.F.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
                                                                                                                                                      A;Cross-references: EMBL:U43703; NID:g1244769; PIDN:AAB68221.1; PID:g1244776; MIPS:YPL135
C;Genetics:
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R, anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A;Residues: 1-743 <VAN>
A;Cross-references: EMBL;Z28292; NID:g486536; PIDN:CAA82146.1; PID:g486537; MIPS:YKR067w
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C.Species: Xylella fastidiosa
C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: S3813,
R;van Vliet-Reedijk, J.C.; Planta, R.J.
R;van Vliet-Reedijk, J.C.; Planta, R.J.
A;Reference number: S38130
                                                                                                                                                                                                                                                                      A;Cross-references: SGD:S0006060; MIPS:YPL139c
A;Map position: 16L
C;Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
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Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches
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Pred. No. 43;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: SGD:S0001775
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Best Local Similarity 75.0
Matches 6; Conservative
A; Reference number: S69040
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85 IVPLGLHY 92
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                             A, Accession: S69046
A, Molecule type: DNA
A, Residues: 1-460 <HAL>
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'I protein - tobacco yellow dwarf virus (strain Australia)

C;Species tobacco yellow dwarf virus

C;Species tobacco yellow dwarf virus

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999

C;Accession: A42452

C;Accession: A42452

C;Accession: A42452

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85046
hypothetical protein YPL139c - yeast (Saccharomyces cerevisiae)
c;Species: Saccharomyces cerevisiae
c;Species: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
C;Accession: 869046
C;Accession: 869046
R;Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 9, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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                                                                                                                Gaps
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                             66.1%; Score 37; DB 2; Length 1057; 60.0%; Pred. No. 39;
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                                                                                                                2; Indels
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                                                                                                            2; Mismatches
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Best Local Similarity 60.0*
                                                                  Best Local Similarity 60.0
Matches 6; Conservative
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235 EMIVPAGLHF 244
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A; Residues: 1-102 <MOR>
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A;Status: preliminary
A;Molecule type: DNA
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                             Query Match
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219 EEVVESGLHES 229
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C;Specials Micotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
C;Date: 05-Mar-1999 #sequence property in the property of the plant of the plan
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A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Acdrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, T.R.; da Silvai, A.M.; Silva Jr., W.A.; da Silvai, F.R.; da Silvai, A.M.; Silvai Jr., W.A.; da Silvai, A;Reference number: A59328

A;Reference number: A59328

C;Genetics:
A;Gene: XF1950
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A,Cross-references: GB:AE000850; GB:AE000666; NID:g2621794; PIDN:AAB85215.1; PID:g262179
A,Experimental source: strain Delta H
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Best Local Similarity 55.0-
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Matches 6; Conservative
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Clacession: G86430
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chi, Chung, M.K.; Conn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; M., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                     A, Accession: T24111
A, Status: pre-liminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1.425 < WIL>
A, Cross-references: EMBL; Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP:R10D12.10
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
.
Mypothetical protein R10D12.10 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Pred. No. 45;
2; Mismatches 2; Indels
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Pred. No. 37;
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C,Superfamily: hexose phosphate transport protein uhpT
                                                                                                                                                                       submitted to the EMBL Data Library, October 1996
A;Reference number: Z19842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 23/3; 56/3; 113/3; 257/2
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50.0%;
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60.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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A; Residues: 1-510 <STO>
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C; Genetics
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R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; J. Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. S.; Curch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 1135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Accession. G69117
A; Accession. A; Mullips acid sequence not shown; translation not shown A; Mesidues: 1-264 cMTH>
A; Residues: 1-264 cMTH>
A; Residues: 1-264 cMTH>
A; Experimental source: strain Delta H
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C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C.Accession: C7558
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Vaneter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Reference number: A75250; MuID:20036896; PMID:10567266
A.Accession: C75538
A.Accession: Preliminary
A.Accession: L279 <WHI>
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A;Experimental source: strain R1
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A;Gene: DR0271
A;Map position: 1
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A;Cross-references: GB:AE001932, GB:AE000513; NID:g6458481; PIDN:AAF10353.1; PID:g6458486 A;Experimental source: strain R1 C;Genetics: C;Genetics: A;Gene: DR0777 A;Map position: 1 C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Streptomyces coelicator
Cispecies: Streptomyces coelicator
Cispate: 05.Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
Ciscession: T35025
Riseger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, June 1999
A;Reference number: 221565
A;Reference number: 221565
A;Reference number: Arguniary; translated from GB/EMBL/DDBJ
A;Reference number: 135025
A;Reference number: 22156
A;Reference number: 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2; Length 350;
Pred. No. 48;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable DNA ligase - Streptomyces coelicolor
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Job time : 12 secs
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Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 EAVAYGMHYA 261
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June 4, 2003, 13:09:19; Search time 9.75 Seconds (without alignments) 33:195 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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56
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                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                               Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cri	94 Seguence 4794, Ap	19. Ar	2 .			Sequence 23, Appl		'n	Sequence 4, Appli	4	4	Sequence 7, Appli	21.	21.	N	21,	22,	22	0	22,	9	9	4	Sequence 4, Appli	9	Sequence 23. Appl	,
SUMMARIES	ID	US-09-134-001C-47	US-08-821-119-19	-08-821-118-2	US-09-724-864-36	-39	-988A-2	US-08-879-995A-3	US-09-215-096-3	US-08-460-694-4	US-08-460-744-4	US-07-667-711B-4	US-08-193-977-7	US-08-464-517-21	US-08-246-361A-21	US-08-463-772-21	PCT-US93-05000-21	US-08-464-517-22	US-08-246-361A-22	US-08-463-772-22	PCT-US93-05000-22	US-08-464-517-6	US-08-463-772-6	US-08-246-361A-4	PCT-US93-05000-4	PCT-US93-05000-6	US-08-464-517-23	US-08-246-361A-6
	Length DB		600 2	600 2	747 4	70 4	•	•	126 3	•	152 3	•								236 3								
<b>%</b>	Query	9.69	60.7	60.7	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
	Score	39	34	34	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
	Result No.	1	7	m	4	S	9	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

GENERAL INFORMATION:

APPLICANT: Holm, Kaj Andre

APPLICANT: Rasmussen, Grethe

APPLICANT: Halkier, Torben

APPLICANT: Lehnbeck, Jan

TITLE OF INVENTION: Tripeptidyl Aminopeptidase

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc.

STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:

STREET: 405 Les CITY: New York

RESULT 2 US-08-821-119-19 Sequence 19, Application US/08821119 Patent No. 582104

1 EEVVPXGMHYS 11

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28 32 57.1 292 2 US-08-246-361A-23 Sequence 30 32 57.1 292 5 US-08-246-361A-23 Sequence 31 32 57.1 292 5 PCT-US93-05000-23 Sequence 32 32 57.1 292 5 PCT-US93-05000-23 Sequence 32 32 57.1 295 1 US-09-460-694-2 Sequence 32 32 57.1 295 1 US-09-460-694-2 Sequence 33 2 57.1 295 2 US-08-444-377-29 Sequence 34 32 57.1 295 2 US-08-444-377-29 Sequence 35 57.1 295 2 US-08-444-377-29 Sequence 37 32 57.1 295 2 US-08-444-377-20 Sequence 37 32 57.1 295 2 US-08-444-377-20 Sequence 39 32 57.1 295 2 US-08-444-377-20 Sequence 45 32 57.1 295 3 US-08-46-561A-29 Sequence 45 32 57.1 295 3 US-08-46-561A-29 Sequence 47 32 57.1 295 3 US-08-46-517-20 Sequence 47 32 57.1 295 3 US-08-46-517-20 Sequence 47 32 57.1 295 5 PCT-US93-05000-2 Sequence 47 34 Application US/09134001C Sequence 47 34 Application US/09134 Sequence 47 34 Application US/09134 Sequence 47 34 Application US/09134 Sequence
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APPLICANT: Rey, Michael
APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPPETIDE AMINOPEPTIDASE
TITLE OF INVENTION: ACTIVITY
CORRESPONDENCE: ACCOUNTY
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59898890 No. 5989889disk of No. 5989889th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 15-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08821118 Patent No. 5989889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 Lexington Avenue
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 411
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                         600 amino acids
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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PACENTAL INCORPATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/09724864
Patent No. 6580362
Patent No. 6580362
GENERAL INFORMATION:
APPLICANT: Murison, James D
APPLICANT: Murison, James D
TITLE OF INVENTION: Polynuclectides and methods for their use.
TITLE OF INVENTION: Polynuclectides and methods for their use.
FILE REFERENCE: 11000.105011
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT PILING DATE: 2000-11-28
PRIOR PILING DATE: 1999-12-23
NUMBER: OF SEQ ID NOS: 72
CORPERING PART: 1999-12-23
NUMBER: OF SEQ ID NOS: 72
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                                                                                                                                          Score 34; DB 2; Length 600;
Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                            0; Mismatches
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FastSEQ for Windows Version 4.0
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                                                                                                                                                 60.7%;
                                                                                                                               Query Match
Best Local Similarity 75.v.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 PGGLHYS 633
                                                                                                                                                                                                                                         4 VPXGMHYS 11
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Matches 5; Conserva
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ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Fas
SEQ ID NO 36
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-724-864-36
                                                                                                          US-08-821-118-2
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US-08-580-988A-23
Sequence 23, Application US/08580988A
Sequence 23, Application US/08580988A
Setent No. 5856161
GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
TITLE OF INVENTION: For Its Use
UNUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hall preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICALL...

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-6908
; INFORMATION FOR SEQ ID NO: 23:
SEQUIENCE CHARACTERISTICS:
SEQUIENCE CHARACTERISTICS:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER NAMBORIES TOWN:
WEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION: 424
PROR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08879995A Patent No. 5985606 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIRCANO.
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
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MEDIUM TYPE: 1.44 MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 EEVFPLAMNY 33
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                      :| | | | | 36 MPKGFHYS 43
4 VPXGMHYS 11
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; FRAGMENT TYPE: i
; ORIGINAL SOURCE:
US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             77071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION
APPLICANT: Ital, Preeti
APPLICANT: Kaeer, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS SOFTWARE: FASTSEN OF Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/879,995A FILING DATE: Herewith CLASSIFCTATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0326 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPREDENCE/DOCKET NUMBER: PP-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.1
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDLL
TOPOLOGY: 111.
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 EQVVPGGGH 36
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EEVVPXGMH 9
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STATE: CA
                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-215-096-3
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                                   3; Indels
                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08460744

Patent No. 6107541

GENERAL INFORMATION:
APPLICANT: AAROLIGA Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
INUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and Its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE SESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTKI: ...
ZIN: 20005
ZIF: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: BY PC COMPATIBLE
OFFWARE: PATEMIN PC-DOS/MS-DOS
SOFFWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
TITING DATE: ...
435
60.0%; Pred. No. 44; tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCCOnathy, Evelyn H.
REGISTRATION UNDRER: 35,279
REFRENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEBHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
Best Local Similarity 60.0
Matches 6; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
                                                                                              1 EEVVPXGMHY 10
                                                                                                                                                            20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EEVVPXGMHY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
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STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20005
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                                                                                                                                                                                                                                                                                 US-08-460-744-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 32; DB 2; Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD! Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY UGA

ZIP: 20005

COMPUTER READELE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 0.2-JUN-1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: MACCONCAIN, Evelyn H.
REGISTRATION NUMBER: 35,279
REJERENCE/DOCKET NUMBER: 0609.4070002
TELEFAN: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEMETHE FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEMETHE FAILS AMILE AS A SECONDER AND A SEQUENCE CHARACTERISTICS:
LEMETHE FAILS AMILE AS A SECONDER AND A SEQUENCE CHARACTERISTICS:
LEMETHE FAILS AND A SECONDER AND A SEQUENCE CHARACTERISTICS:
LEMETHE FAILS AND A SECONDER AND A SEQUENCE CHARACTERISTICS:
LEMETHE FAILS AND A SECONDER A
                                                                                                                                           NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: Genbank CLONE: 163590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 EQVVPGGGH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPXGMH 9
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-215-096-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-460-694-4
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FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-0CT-1992

APPLICATION NUMBER: US 07/888,178

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514

FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent

REGISTATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MII-004C

TELEFANO: (617) 227-7400

TELEFANO: (617) 227-7401

TELEFANO: (617) 227-7401

TELEFANO: (617) 227-7401

TELEFANO: (617) 227-541

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTER/SITICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-246-361A-21
; Sequence 21, Application US/08246361A
; Patent No. 5998582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60..
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                      1 EEVVPXGMHY 10
                                                                                                                                                                                                              55 EEVFPLAMNY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 EEVFPLAMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
                                                                                                                                                                                                                                                                                                        US-08-464-517-21
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                                  US-08-193-977-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 940N 405K
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DAM PC COMPAINS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%; Score 32; DB 3; Length 152; 60.0%; Pred. No. 44; tive 1; Mismatches 3; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OF/667,711B
FLING DATE: II-MAR-1991
CLASSIFICATION: 435
ATTONREY/AGENT INPOMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REGISTRATION NUMBER: 35,811
REGISTRATION NUMBER: 35,810
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
TELEPAK: (202) 371-2540
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 277-8999
TELEPHONE: (415) 277-8999
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08193977 Patent No. 5625031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: not relevant; MOLECULE TYPE: peptide US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEVVPXGMHY 10
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Patent No. 5865640
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
Query Match 57.1%; Score 32; DB 1; Length 173; Best Local Similarity 60.0%; Pred. No. 51; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%; Score 32; DB 2; Length 189; 60.0%; Pred. No. 56; 3; Indels tive 1; Mismatches 3; Indels
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Gaps
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US-08-463-772-21
$$ 'Sequence 21, Application US/08463772$
$$ 'Sequence 21, Application US/08463772$
$$ 'Batent No. 6066501$
$$ GENERAL INFORMATION:
$$ APPLICANT: BEACH, David H.
$$ TITLE OF INVENTION:
$$ NUMBER OF SEQUENCES: 50
$$ CORRESPONDENCE ADDRESS:
$$ ADDRESSEE: LAHIVE & COCKFIELD
$$ STREET: 60 State Street
$$ STREET: 80 State
$$ STREET: MA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
INVMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: BOSCON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

57.1%; Score 32; DB 2; Length 189;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                     COUNTRY: UGA
ZIP: 02109
COUNTRY: UGA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFTCATION ATA:
APPLICATION DATA:
APPLICATION UMBER: US 07/963,308
FILING DATE: 16-CT-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
FELECOMMUNICATION INFORMATION:
TELEFONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SUBGUENCE CHRARACTERISTICS:
LENGTH: 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC COMPATIBLE
COMPUTER: ON SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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Gaps
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Pred. No. 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
APPLICATION NUMBER: US 07/701,514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     36,709
ER: MII-004C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: June 4, 2003, 13:14:59
Job time : 10.75 secs
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                   NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: MI.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0°
Solution 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-463-772-21
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMHY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                      (without alignments)
51.885 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcgdata/geneseg/genesegp-emb1/AA1993.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT
                                                                                                                                                                                  June 4, 2003, 13:04:09; Search time 28.25 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Geneseq 101002:*
1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                        1 eevvpxgmdys 11
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                                                                                                                                                                                                                                                                                                             AUDET-909-3
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                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database:
                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Resu
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					SUMMARIES	
		dф			•	
sult		Query				
No.	Score	Match	e Match Length D	8	ID	Description
1 /	52	96.3	11	23	ABB80524	Hepatitis C virus
~ -	52	96.3	11	23	ABB80528	Hepatitis C virus
m	52	96.3	11	23	ABB80529	Hepatitis C virus
4	52	96.3	11	23	ABB80561	Hepatitis C virus
2	52	96.3	11	23	ABB80562	Hepatitis C virus
9	47	87.0	11	23	ABB80538	Ü
7	47	87.0	11	23	ABB80542	ΰ
۵	47	87.0	11	23	ABB80543	υ
σ	46	85.2	11	23	ABB80521	O
10	46	85.2	11	23	ABB80522	Hepatitis C virus

Hepatitis C virus	
23 ABB80525 23 ABB80547 23 ABB80547 23 ABB80556 23 ABB80556 23 ABB80556 23 ABB80556 23 ABB80563 23 ABB80564 23 ABB80567 23 ABB80567 23 ABB80567 23 ABB80567 23 ABB80567 23 ABB80568 23 ABB80523 23 ABB80533	ABB80553 ABB80553 ABB80554 ABB80554 ABB80554 ABB80553 ABB80553 ABB80553 ABB80553 ABB80553 ABB80553 ABB80553 ABB80553 ABB80553
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. C C C C C C C C C C C C C C C C C C C
11111111111111111111111111111111111111	

## ALIGNMENTS

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/note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
                                                                                                                                                                     note= "N-terminal acetyl"
                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                        /note= "D-form residue"
                                                                                                                                                Location/Qualifiers
                  ABB80524 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                      19-JUL-2001; 2001WO-US23169.
                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-220101P.
                                                          08-OCT-2002 (first entry)
                                                                                                                                                                                                             Misc-difference 9
                                                                                                                                                                                                                                                              WO200208251-A2
                                                                                                                                                    Key
Modified-site
                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                  31-JAN-2002.
                                                                                                                               Synthetic.
                                      ABB80524;
RESULT 1
ABB80524
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activity useful for treating disorders associated with hepatitis C
                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus protease
            virus protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                       Addified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000;
                                                                                                                                                                                                                                                                                         08-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                            Sequence
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                       ABB80529
                                                                                                                                                                Matches
                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                            ABB80529
  FFX8XX0000000X8
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                                                                                                                                                                                                                                           ö
                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Norvalyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                 Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noval peptide compound having hepatitis C virus protease inhibitory
                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8
                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                      96.3%; Score 52; DB 23; Length 11; 100.0%; Pred. No. 0.0015; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                            Brunck TK;
                                                                                                                                                                                                                                                                                                                           ABB80528 standard; peptide; 11 AA
                                                                                                      Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000US-220101P.
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                            1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                              EEVVPXGMDYS 11
         CORVAS INT INC.
                            Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lim-wilby M, Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-361643/39.
                                              WPI; 2002-361643/39
                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                    11 AA;
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                                                                                     virus protease
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                            Lim-wilby M,
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                                                                                                                                                                                                                                                                                                                                                                                                                virucide.
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          (CORV-)
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  96.3%; Score 52; DB 23; Length 11; 100.0%; Pred. No. 0.0015; ive 0; Mismatches 0; Indels
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Claim 17; Page 64; 69pp; English
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nes 11; Conservative
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             invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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    residue 7"
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
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                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
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                                                                                                                                   96.3%; Score 52; DB 23; Length 11; 100.0%; Pred. No. 0.0015; rive 0; Mismatches 0; Indels
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                                                                                                                                      Query Match 96.3
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                         11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     "Norvalyl carbonyl forming keto-amide linkage with
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                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
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                    ; DB 23; Lens.
o. 0.0015; Indels
                                 Length 11;
                                          100.0%; Prec. ...
'''e 0; Mismatches
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                                 Score 52;
Pred. No.
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                                                                                                                                                                       ABB80562 standard; peptide; 11 AA.
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                                   96.38;
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                                                          11; Conservative
                                                                                   1 EEVVPXGMDYS 11
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           11 AA;
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Best Local &
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                                                                                                                                             RESULT 5
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DB 23; Length 11;

96.3%; Score 52;

Query Match

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08-OCT-2002
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                                              ABB80542;
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                                                                                                                                                                                                                                                      /note= "Norvalyl carbonyl forming keto-amide linkage with
                   Gaps
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                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
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Pred. No. 0.014;
0; Mismatches 1; Indels
100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                      /note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                               residue 7"
                                                                                                ABB80538 standard; peptide; 11 AA.
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                                                                                                                                   (first entry)
                  11; Conservative
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                                            1 EEVVPXGMDYS 11
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                                    1 EEVVPXGMDYS
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ABB80538
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                                                                                                                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
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ABB80542 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-361643/39.
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virus protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                           "Norvalyl carbonyl forming keto-amide linkage with
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                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1
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                                                                                                                    'note= "N-terminal acetyl"
                                                                                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                               /note= "D-form residue"
                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English.
                                                                                                                                                                                                                                                                                                                        19-JUL-2001; 2001WO-US23169
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les 10; Conservative
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                                                                                                                                                /note=
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Modified-site
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Matches
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                                                                    carbonyl forming keto-amide linkage with 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
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                                          'note= "N-terminal acetyl"
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Pred. No.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                Brunck TK;
                                                                                       "Norvalyl
residue 7
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/note= '
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                                                                                           /note=
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Best Local Similarity
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21-JUL-2000; 2000US-220101P.
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                                                                                          virus protease
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                                    Lim-wilby M,
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                                                                                                                                            Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                sequence represents a peptide compound of the invention having
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
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                                                                                                                                                                                                                                                                                          Score 46; DB 23; Length 11;
Pred. No. 0.022;
0; Mismatches 1; Indels
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/note= "C-terminal amide"
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                                                                                                           Brunck TK;
                                                                                                                                                                                                                                                                                                                                                                                           ABB80525 standard; peptide; 11 AA.
                                                                                                                                                                                Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                          85.2%;
90.9%;
                                                                       21-JUL-2000; 2000US-220101P.
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                                                    19-JUL-2001; 2001WO-US23169
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                          Lim-wilby M, Levy OE,
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                                                                                        (CORV-) CORVAS INT INC
                                                                                                                            WPI; 2002-361643/39.
                                                                                                                                                                virus protease -
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                      Brunck TK;
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(CORV-) CORVAS INT INC
                                                      Levy OE,
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                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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0.022;
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/note= "C-terminal amide"
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Pred. No.
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                                                                               Claim 17; Page 64; 69pp; English.
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                                                                                                                                                                                                                                                85.2%;
90.9%;
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Best Local Similarity 90.5.,
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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WPI; 2002-361643/39
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                                                    protease
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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    residue 7"
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ilarity 90.9%;
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 Score 46; DB 23; Length 11;
Pred. No. 0.022;
0; Mismatches 1; Indels
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85.2%;
90.9%;
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 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                        1 EEVVPXGMDYS 11
                                                                      (CORV-) CORVAS INT INC
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Gaps

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Search completed: June 4, 2003, 13:11:13 Job time: 28.25 secs

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212479
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030260 archaeoglob
08rg86 fusobacteri
022081 citrus unsh
022096 citrus unsh
08w568 arabidopsis
09c9t7 arabidopsis
09c9t7 arabidopsis
09c9t0 oryza sativ
08s064 oryza sativ
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Q8xpa8 clostridium
O52367 rhizobium t
Q9xvk4 caenorhabdi
Q9a382 caulobacter
                                                                                                   4, 2003, 13:07:09; Search time 22.5 Seconds (without alignments) 100.734 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                    671580
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                            671580 segs, 206047115 residues
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m	Q9YFI3	17	440	4.	35	17

### ALIGNMENTS

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STRAIN=FY1679;
MEDLINE=94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sherman F.; "CYC2 encodes a factor involved in mitochondrial import of yeast
                                                                                                                                                                                                                                                                                                                                                                  De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                         Last sequence update)
Last annotation update)
                                                     156 AA
                                                                                                     Created)
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Mol. Cell. Biol. 13:6442-6451(1993).
                                                PRT;
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MEDLINE=94169519; PubMed=7764548;
                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, ORF YOR013W.
                                                     PRELIMINARY;
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RESULT 1
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SEQUENCE
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Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 58:391-395 (1994).

EMBL; Z74920; CAA697201.1; -.
SGD; S0005539; YOR033w.
SCDUBNCE 156 AA, 17881 MW; 380442B74C272B41 CRC64;
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                                                                                                                                                                                                    74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 1.7;
                                                                                                                                                                                                                                                  1; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last amnotation update)
earbamoyl-phosphate synthase large chain (EC 6.3.5.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI TaxID=2234;
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                                                                                                                                                                                                                                                  1; Mismatches
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EMBL; AE001109; AAB91255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein AF2411.
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Best Local Similarity 54...
Best Local Similarity 64...
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Matches 7; Conservative
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01-MAR-2002
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BMBL; AB006319; BAA23215.1; -.
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                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 2586;
MEDLINE=21886394; PubMed=11889109;
MEDLINE=21886394; PubMed=11.899109;
MEDLINE=21886394; PubMed=11.809109;
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25866."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. MIYAGAWA-WASE; TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
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Komatsu A., Takanokura Y., Omura M., Akihama T.; three sucrose
"Cloning and moleoular analysis of cDNA encoding three sucrose
phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%; Score 38; DB 16; Length 1063; 60.0%; Pred. No. 39;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria, Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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EMBL; AE010554; AAL94625.1; -.
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195 EIVPNGLNYS 204
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                                                               NCBI_TaxID=76856;
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49682 MW; A159955B21742C4A CRC64;

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452 AA;
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TISSUE-JUICE SACS AND SEGMENT EPIDERMIS;
Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
Formatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
Plant Sci. 140:169-178(1999).
EMBL; AB006660; BAA22071.1; -.
                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Sapindales, Rutaceae, Citrus.
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96439842; PubMed=8842155;
Komatsu A., Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of cDNA encoding three sucrose
phosphate synthase isoforms from a citrus fruit (Citrus unshiu
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; A419606; AAL31931.; -.
InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR00379; Ser_estrs site.
PROSITE; PS00708; PRO_ENDOPEP_SER; UNKNOWN_1.
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348 348
348 AA, 38556 MW, EEIC21EBAGFFSC5E CRC64;
                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
At1g73750/F25F22_17.
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TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
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                                                 PRT;
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                                                                                                                                                                                                            Citrus unshiu (Satsuma orange).
                                                 PRELIMINARY;
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022096
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SEQUENCE FROM N.A.

SEQUENCE TO COLUMBIA,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Browman C.L., Brooks S.Y.,

White O., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A cill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A cill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A cill J.E., Goldsmith A.D., Lanson Hopson C., Khan S., Khaykin B.,

Kim C.J., Koo H.L., Kemenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Naiti R., Marziali A.,

Nai G., Peterson J., Pam P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Nu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702,
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Length 452;
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Pred. No. 41;
0; Mismatches 3; Indels
                                                                Indels
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InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR00379; Ser_estre site.
PROSITE; PS00708; PRO_ENDOPEP_SER; UNKNOWN_1.
PROSITE; PS04708; PRO_ENDOPEP_SER; UNKNOWN_1.
SEQUENCE 460 AA; 50564 MW; E94B27BSC4B249EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 50.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAX-2002 (TrEMBLrel. 20, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment)
                                                                3,
   DB 10;
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                                                                                                                                                                                                                                                                                                                                                460 AA.
                                                                0; Mismatches
                                   40;
Score 36;
Pred. No.
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   66.7%;
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70.0%;
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Best Local Similarity 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 408:816-820(2000).
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Query Match
Best Local Similarity
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Conservative
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                                         01-NOV-1996 (TrEMBLrel.
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ses 6; Conserv
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                                                                                                                                                                       NCBI_TaxID=4530;
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             Q43010
Q43010;
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                                                                                                          Sugilation B., Sakakibara H., Sugiyama T.;
Sugilation B., Sakakibara H., Sugiyama T.;
Differential Expression of Two Genes for Sucrose-Phosphate Synthase in Sugarcane: Molecular Cloning of the CDNAs and Comparative Analysis of Gene Expression. The EMBL/GenBank/DDBJ databases.

EMBL, AB001337; BAA19241.1;
EMBL, AB001396; Glycos transf_1:
Pfam; PF00554; Glycos transf_1:
Pfam; PF00554; Glycos transf_1:
Glycosyltransferase; Transferase.
             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Saccharum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MXY-2000 (TrEMBLrel. 13, Created)
01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-MXY-2000 (TrEMBLrel. 20, Last annotation update)
01-MXR-2002 (TrEMBLrel. 20, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
P28M11.40 OR AT4G10120.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL; AL049487; CAB39764.1; -
EMBL; AL161516; CAB78135.1; -
InterPro; IPR01296; Glycos transf_1.

Ffam; PF00534; Glycos transf_1; 1.

Glycosyltransferase; Transferase.

SEQUENCE 1083 AA; 122688 MW; EFC126FCA2137BBI CRC64;
                                                                                                                                                                                                                                                        SEQUENCE 1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1083 AA.
                                                                                                                                                                                                                                                                                                                2; Mismatches
Saccharum officinarum (Sugarcane)
                                                                                                                                                                                                                                                                                     66.7%;
                                                                                                                                                                                                                                                                                                                6; Conservative
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hes 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       414 VIPPGMDFS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                            3 VVPXGMDYS 11
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                                                        NCBI_TaxID=4547;
                                                                                                 TISSUE=LEAF;
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RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                               Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Sukaryota, Vitidplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Sasaki I., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.7%; Score 36; DB 10; Length 1084; Best Local Similarity 66.7%; Pred. No. 1.18+02; Matches 6; Conservative 2; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ECV. JAPONICA;
Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Fujimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone:P0679F11.";
Submitred (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003437; BAB86107.1; -
SEQUENCE 1100 Aa; 121170 WW; 084F4604BA389CAD CRC64;
                                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
L-lactate dehydrogenase (EC 1.1.1.27) (LDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-UUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1084 AA.
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                                               Created)
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P0678F11.14.
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469 VIPPGMDFS 477
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RESULT 14
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                                                                                                                                                                                                                                        TISSUE-GILL;
which can be made b.w.;
which can be made b.w.;
which can be considered by the contraresporter are expressed in gills of the euryhaline Chinese crab Eriocheir sinensis.";
Comp. Blochem. Physiol. 126:8158-8158(2000).
EMBL; AF301160; AAG39938.1; --
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0
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.8%; Score 35; DB 16; Length 253; 50.0%; Pred. No. 34; Live 3; Mismatches 2; Indels
                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Na+/K+/2Cl-cotransporter (Fragment)
Eriocheir sinensis (Chinese mitten crab)
Eukaryota, Metazoa, Arthropoda, Crustacea; Malacostraca;
Eumalacostraca; Eucarida, Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
                                                                                                                                                                                                                                                                                                                                                                                         64.8%; Score 35; DB 5; Length 219; 75.0%; Pred. No. 29; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003185; BAB7973.11, -
InterPro; IPR0000594; This domain.
Pfam; PF00899; This; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 253 AA; 27714 WW; 814DF79D3E0D7486 CRC64;
                                                                                                                                                                                                                                                                                                                                                               219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein CPE0057.
                                               219 AA.
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Best Local Similarity 50.07
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Best Local Similarity 75...
6; Conservative
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108 EEIIPDDVDY 117
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STRAIN=13 / TYPE A;
PubMed=11792842;
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1502;
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SEQUENCE
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                  RESULT 12
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Rosenblueth M., Hynes M.F., Martinez-Romero E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: ZINC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                 Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group, Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.8%; Score 35; DB 2; Length 298; 50.0%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percy C.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             NON TER 298 298 SEQUIENCE 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
R10D12.10.
                                  Created)
Last sequence update)
Last annotation update)
                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence upda
01-JMR-2002 (TrEMBLrel. 20, Last annotation upda
Alryl-alcohol dehydrogenase homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Z81109, CAB03241.1;
InterPro, IPR00719; Buk pkinase.
Pfam, PF00069; pkinase; 1.
ProDom, PD000001; Euk pkinase; 1.
PROSTTE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                          EWBL; AF036920; AAC04779.1; -.
HSSP; P07846; ISDG.
InterPro; IRR002328; ADH_zinc.
InterPro; IRR0023085; Adh_zn family.
InterPro; IRR002005; NAD_binding.
Pfam; PF00107; adh_zinc; 1.
Oxidoxeductase; Plasmid; 2.
NON TER 298 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::| | |:|
250 EIIPEGADFS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EVVPXGMDYS 11
                                                                                                                          Plasmid pRtrCFN299a.
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                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                         Rhizobium tropici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                               NCBI_TaxID=398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XVK4;
                         052367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09XVK4
           052367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
Q9XVK4
052367
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Page 6

audet-909-3.rspt

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0
                                                          0; Gaps
Query Match 64.8%; Score 35; DB 5; Length 425; Best Local Similarity 50.0%; Pred. No. 61; Matches 5; Conservative 3; Mismatches 2; Indels
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1 EEVVPXGMDY 10 |::|| |: || 335 EQIVPGGLQY 344 ر م

Search completed: June 4, 2003, 13:13:26 Job time: 23.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:04:34; Search time 6.25 Seconds Run on:

(without alignments)
72.998 Million cell updates/sec

1 eevvpxgmdys 11 Perfect score: Sequence:

AUDET-909-3

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARIES

		Description .	Q8rg86 fusobacteri	P31619 tobacco yel	Q43802 oryza sativ	P31927 zea mays (m			O9nr64 homo sapien		hordeum		3 borreli		pseudon			_			_	-	7	m	ი	N	C)	Ň	_	m		Q9wzr1 thermotoga	_	0279	P30280 mus musculu
SUMMARIES		ID	CARB FUSNN	Y11K_TYDVA	SPS ORYSA	SPS MAIZE	SPSZ CRAPL	FAF DROME	KHL1 HUMAN	PLAS_ORYSA	PLAS_HORVU	PLAT_POPNI	SYFB_BORBU	Y939 METUA	PANC_PSEAE	HMPA_VIBCH	ACDM RAT	ECB2_HALEL	ECB1_HALEL	ECE2_HUMAN	FGR3 MOUSE	CEK2_CHICK	SULH SCHPO	ENV SFV3L	RPOC_VIBCH	ZEP1 HUMAN	ET2A_XENLA	PLAS DAUCA	HES3 RAT	ARAD ECOLI	ARAD_SALTY	HIS9 THEMA	CGD2_RAT	CGD2_HUMAN	CGD2_MOUSE
		DB	1	Н	Н	Н	н	7	Н	П	Н	Н	Н	Н	Н	Н	Н	Н	Н	H	Н	-	Н	Н	Н	٦	Н	7	Н	Н	Н	7	Н	Н	Н
		Match Length	1058	102	1049	1068	1081	2747	748	154	155	168	999	276	283	394	421	421	423	787	801	806	877	982	1401	2717	472	97	175	231	231	233	288	289	289
	* Ouery	Match	. 0	66.7	66.7	66.7	66.7	64.8	63.9	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	60.2	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3
		Score	(1)	36	36	36	36	35	34.5	34	34					33			33				33		33	33			32			32		32	32
	Result	No.	1	7	m	4	Ŋ	9	7	89	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

PROSITE; PS00866; CPSASE\_1; 2.

Q90459 brachydanio	P50755 xenopus lae	P49706 gallus gall	P53782 xenopus lae	P55169 gallus gall	P30281 homo sapien	P24385 homo sapien	P25322 mus musculu	P39948 rattus norv	O30640 methanosarc	Q91712 xenopus lae	
CGD1_BRARE	CGD1 XENLA	CGD2_CHICK	CGD2_XENLA	CGD1_CHICK	CGD3 HUMAN	CGD1 HUMAN	CGD1 MOUSE	CGD1_RAT	MTBA_METBA	ET2B XENLA	HNFB_XENLA
ч	Н	-	Н	г	ч	Н	н	н	Н	٦	-
291	291	291	291	292	292	295	295	295	338	472	561
59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3
32	32	32	32	32	32	32	32	32	32	32	32
34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=ATCZ 55566

KARAIN=ATCZ 55566

KARAIN=ATCZ 55566

KARAIN-ATCZ 55566

KARAIN-ATCZ 55566

WEDLINE-21886394; PubMed=11889109;

KARAIN-ATCZ 55566

MEDLINE-21886394; PubMed=11889109;

KARAIN-ATCZ 55566

MARTINATIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + Discoperation - Corperation - Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Arginine biosynthesis, first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
-!- SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)
                                                                                                                                                                                                                                                                                                                                     Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE010554, AAL94625.1; ALT_INIT.
InterPro; IPR005493; CPase L.
InterPro; IPR005499; CPase L.D2.
InterPro; IPR005490; CPase L.D3.
InterPro; IPR005490; CPase L.D3.
InterPro; IPR005491; CPase L.N.
InterPro; IPR005491; CPase L.N.
InterPro; IPR005491; CPase L.Chain; Pfam; PF02786; CPase L.Chain; Pfam; PF02786; CPase L.D2; 2.
Pfam; PF02786; CPase L.D3; 1.
Pfam; PF02786; CPase L.D3; 1.
Pfam; PF02786; CPase L.D3; 1.
                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                         CARB OR FN0422
                                                                   FUSIN
                                                                                            QBRGB6;
                                   CARB_FUSNN
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonous plants.";
                                                            OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                   ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
              Arginine biosyntnesis, it. The proteome.

ATP-binding; Manganese; Complete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
                                                                                                                                                                                                                                                                                                           ;
0
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0
                                                                                                                                                                                                                                                                          Score 38; DB 1; Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 36; DB 1; Length 102; 60.0%; Pred. No. 1.7; 1.7; 1.4e 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                               MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR002621; Gemini mov.
Pfam; PF01708; Gemini mov; I.
Hypothetical protein.
SEQUENCE 102 Aa; 11178 MW; A40ECFIE0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              102 AA
                                                                                                                                                                                                                                                                                        Pred. No. 7.8;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                             70.48;
                                                                                                                                                                                                                                               117451
                                                                                                                                                                                                                                                                                      60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                        Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  190 EIVPNGLNYS 199
                                                                          929
1058
546
1058
                                                                                                                                                                                                                                                                                                                                      2 EVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVVPXGMDYS 11
                                                                                                                                                                                                                                            1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssDNA vir
                                                                                                                                                                                                                                                                                                                                                                                                                             YIIK_TYDVA
ID YIIK_TYDVA
AC P31619;
                                                                                                      REPEAT
REPEAT
NP_BIND
NP_BIND
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                            DOMAIN
                                                                                        DOMAIN
                                                                                                                                                                                                                             METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Sucrose synthesis.
-!- SUBLINIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
-!- FUNDENPORTATED. HOMEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.

-i- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sucrose 6-phosphate.
ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annocation update)
15-DEC-1998 (Rel. 37, Last annocation update)
15-DEC-1998 (Rel. 37, Last sunctation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Indica-IR36; TISSUE=Leaf;
MEDLINE=96235138; PubMed=8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U311/5; AAC+35/2.1.
InterPro; 1PR001296; Glycos transf_1.
Pfan: PF00534; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
22
29
POLY-GLY.
      PRT; 1049 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1068 AA.
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SPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U33175; AAC49379.1; -.
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 170:217-222(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 VIPPGMDFS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herrera-Estrella L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
SPS ORYSA
Q43802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPS_MAIZE
P31927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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RESULT 3

audet-909-3.rsp

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SOUTH THE TRANSPORT OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Lamiales, Lamiales incertae, sedis, Torenieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
-!- DEVELOPMENTAL STAGE: GERMINATING SEEDS OR MATURE LEAVES.
-!- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                 STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=92338837; PubMed=1840396;
Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A.;
"Expression of a maize sucrose phosphate synthase in tomato alters
leaf carbohydrate partitioning.";
Plant Cell 3:1121-1130(1991).
                                                                                                                                                                                                                                                                                                           FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THERREPORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-
                                                                                                                                                                                                                                                                                                                                                                                                                               SUCTOSE 6-Phosphate.
ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
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SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 36; DB 1; Length 1068; 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1081 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1068 AA; 118575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate glucosyltransferase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Sucrose synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M97550; AAA33513.1; -. PIR; JQ1329; JQ1329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craterostigma plantagineum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 VIPPGMDFS 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                      NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craterostigma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          004933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 5
CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
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-!- FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A ROLE IN COMPOUND EYE ASSEMBLY AND OOGENESIS RESPECTIVELY. IN THE LARVAL FYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR
                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Sucrose synthesis.
-!- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
-!- POSPHORYLATED. HOMEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
(Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease FAF) (Deubiquitinating enzyme FAF) (Fat facets protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001296; Glycos transf 1.
Pfam; PF00534; Glycos transf 1; 1.
Transferase; Glycosyltransferase; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 1081; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   787 790 POLY-ARG.
1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
                                                                                                                                                                                                                                                                                                    sucrose 6-phosphate.
-!- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYL
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93202020; PubMed=1295747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.78;
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Best Local Similarity 60.
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Query Match
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REPEAT
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REPEAT
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REALL, L04958; AAFUL.

REALL, L04958; AAFUL.

RECORS; C19.007; -..

DR FlyBase; FERMO00563; faf.

DR InterPro, IPR001394; UCH-2.

DR PROSITE; PS00973; UCH-2.1; 1.

DR PROSITE; PS00973; UCH-2.2; 1.
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                          ubiquitin + a thiol.

ALTENANTIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: BYE DISKS AND OVARIES.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
                                                          CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIJNE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.,
"The SCA8 transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 2747;
Pred. No. 91;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHL1 HUMAN STANDARD; PRT; 748 AA. Q9NR64; Q9NR65; Q9P238, Q9H4X4; [16-CCT-2001 (Rel. 40, Last sequence update)] 16-CCT-2001 (Rel. 40, Last sequence update)] 16-CCT-2001 (Rel. 40, Last annotation update) RC-1-ke protein 1. KLHL1 OR KIAA1490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20277482; PubMed=10819331;
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1394 EVIVPDGQDFS 1404
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Matches 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissue=Brain;
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                                                                                                                                                                          Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
complete sequences of 100 new cDNA clones from brain which code
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                             -!- SUBCELLUTAR LOCATION: Cytoplasmic.
-! TISSUB SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
-!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.9%; Score 34.5; DB 1;
80.0%; Pred. No. 29;
iive 1; Mismatches 0;
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DT 11-FEB-1991 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DF 15-JUN-2002 (Rel. 41, Last annotation update)
DF 15-JUN-2002 (Rel. 41, Last annotation update)
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PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Repeat.
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KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
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EMBL, AF252279; AAF81716.1; -.
EMBL; AB40903; BAA96014.1; ALT_INIT.
EMBL; AL353738; CAC16128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 605332; -.
'InterPro; IPR000210; BTB_POZ.
InterPro; IPR001798; Kelch.
Pfam; PF00551; BTB; 1.
Pfam; PF01344; Kelch; 6.
PRINTS; PR00501; KELCHREPEAT.
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Lee J.-S.;
                           for large proteins in vitro.";
DNA Res. 7:143-150(2000).
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                                                                                         [3]
SEQUENCE OF 179-409 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     748 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a its content is in no way modified and this statement is not removed. Usage by and for commercial
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Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                                                                                              Protein Seq. Data Anal. 2:385-389(1989).

-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: LOOSELY BOND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.

-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Lilliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                STRAIN=cv. Japonica;
MEDLINE=89386623; PubMed=2780537;
Mano H., Kamo M., Tsugita A., Aso K., Nozu Y.;
"The amino acid sequence of plastocyanin from rice (Oryza sativa,
subspecies japonica).";
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InterPro; IPR001235; BlueCu 1.
InterPro; IPR001235; Copper_blue.
Pfam; PR00127; copper-bind; 1.
ProDom; P000125; COPPERBLUE.
ProDom; P000126; COPPERBLUE; 1.
PROSITE: PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide.

TRANSIT 1. 57 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 154;
Pred. No. 6.8;
2; Mismatches 3; Indels
                                                          Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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01-AUG-1988 (Rel. 08, Last sequence update)
01-UIN-2002 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 155 AA
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Nielsen O.S., Gausing K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 EDAVPSGVDVS 110
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58 1
94 1
139 1
142 1
147 1
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Best Local Similarity
Matches 6; Conserv
                                                                                                                        SEQUENCE OF 58-154
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SEQUENCE
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                                                                                                                            STRAIN=cv. NK 1558;
MEDINE=94033081; Pubmed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Populus nigra (Lombardy poplar).
Bukaryota, Viridiphantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
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                                                                                                                                                                                                                             promoter region.";

Eur. J. Blochem. 217:97-104(1993).

-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: LOCABLY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
"The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues."; FEBS Lett. 225:159-162(1987).
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EMBL; Z28347; CAA82201.1; -.

PIR; S00206, S00206.

InterPro; IPR000923; BlueCu 1.

InterPro; IPR001235; COPPer blue.

Pfam; PF00127; COPPer blud; 1.

PRINTS; PR001235; COPPERBLUE.

PROSTIE; PS001235; COPPER BLUE; 1.

Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 155; Pred. No. 6.9;
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COPPER (BY SIMILARITY).
T - N (IN CV. NK 1558).
W; DAA7EABESF6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Plastocyanin B, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST
                            expression in different tissues.";
Lett. 225:159-162(1987).
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54.5%;
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155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                              [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transit peptide
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLAT POPNI
P11970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POPNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (RC 6.1.1.20) (Phenylalanine--
                                                                            Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
"Complete amino acid sequence of poplar plastocyanin b.";
FBBS Lett. 226.17-22(1987).
-i- FUNCTION: Participates in electron transfer between P700 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 35210 / B31,
Barbour A.G., Hinnebusch J.;
Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and
thioredoxin reductase gene of Borrelia burgdoxferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                          MEMBRANE SURFACE IN CHLOROPLASTS.
-!- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B.
-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                            cytochrome b6-f complex in photosystem I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD001235; Copper Jlue; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family.
1 G9 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 168;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                 Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 AA; 16981 MW; F20DA6EA2038AEEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetales, Spirochaetaceae, Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
Reichert J., Jenzelewski V., Haehnel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P00299; Lruc.
InterPro; IPR000923; BlueCu_1.
InterPro; IPR001235; Copper blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tRNA ligase beta chain) (PheRS)
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z50186; CAA90565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00127; copper-bind; ...
PRINTS; PR00156; COPPERBLUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: || |: |
112 EDAVPSGVDVS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168
106
153
156
                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S00210; S00210.
HSSP; P00299; 1PLC.
                                                             STRAIN=cv. Italica;
Dimitrov M.I., Egoro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                               SEQUENCE OF 70-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHET OR BB0514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYFB BORBU P94283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
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              SEQUENCE FROM N.A.
STRAIR—STCG 35210 ( 1831;
MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterzback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREPANS; TIGRO0471; pheT_arch; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gарв
                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
CHAIN FAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                           diphosphate + L-phenylalanyl-tRNA(Phe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%; Score 34; DB 1; Length 566; 85.7%; Pred. No. 27;
                                                                                                                                                                                                                                  "Genomic seguence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001153; AAC66870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein MJ0939.
MJ0939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U82978; AAB41019.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                    burgdorferi.";
Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03484; B5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 VPFGMDY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VPXGMDY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
SEQUENCE 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rigr; BB0514; -.
                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y939 METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Gmith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCL 1569 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Strover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pantcate--beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
(Pantcate activating enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diphosphate + (R) pantothenate.
-!- PATHWAY: Pantothenate biosynthesis; last step.
-!- SIMILARITY: BELONGS TO THE PANTOTHENATE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.1%; Score 33; DB 1; Length 276; 45.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004886; AAG08116.1; -. InterPro; IPR003721; Pantoate_ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02569; Pantoate ligase; 1.
TIGRFAMs; TIGR00018; panC; 1.
                                                                                                                                                                                                                                                                                                              EMBL; U67537; AAB98946.1; -.
                                                                                                     Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:: ||::|
141 EEIIENGMEHS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               TIGR; MJ0939; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PANC OR PA4730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSEAE
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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PANC_PSEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype O1;
STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
Medelberg J.F. Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 466:477-483(2000).

-!- DOMAIN: CONNISTS OF TWO DISTINCT DOMAINS, ONE IS A HEME-CONTAINING

-CYNGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN

PAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.

-!- SIMILARITY: BELOWGES TO THE GLOBIN FAMILY. TWO-DOMAIN

-!- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00042; globin; 1.
Pfam; PF00175; NAD binding; 1.
Pfam; PF00970; RAD binding 6; 1.
PRINTS; PR00371; FPNCR.
PRINTS; PR00410; PHEMPORALASE.
PROSITE; PS01033; GLOBIN; 1.
Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Flavohemogrotein (Hemoglobin-like protein) (Flavohemoglobin)
                                                    DB 1; Length 283;
                                                                                         2; Indels
               283 AA; 30836 MW; C494949AB40E14E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRON (HEME DISTAL LIGAND)
(BY SIMILARITY).
Pantothenate biosynthesis; Ligase; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxygen transport; Transport; Complete proteome.
DOMAIN 1 136 GLOBIN.
                                                                                                                                                                                                                                                          394 AA.
                                                                                         1; Mismatches
                                                    Score 33; DB
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001834; Cyt. B5_reductase.
InterPro; IPR001709; FPN Cyt_redctse.
InterPro; IPR000971; Globin.
InterPro; IPR001433; Oxred FAD/NAD(P).
InterPro; IPR001221; Phe_hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004358; AAF96096.1; -.
                                                    61.1%;
                                                                      66.7%;
                                                                                       6; Conservative
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                             96 EEMYPDGMD 104
                                                                                                                          1 EEVVPXGMD 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OXIDOREDUCTASES.
                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     HMP OR VCA0183.
Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; VCA0183;
                                                                                                                                                                                                                                                          VIBCH
                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cholerae
                                                                                                                                                                                                                                                          HMPA VIE
Q9KM<u>Y</u>3;
                                                                                                                                                                                                                                       HMPA_VIBCH
                                                                                         Matches
                                                                                                                                                                                                                     RESULT 14
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (Rel. 08, Last sequence update)
15-UTN-2002 (Rel. 41, Last sequence update)
Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor (EC 1.3.99.3) (MCAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: Mitochondrial matrix.
MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-COA DEHYDROGENASES
OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 262:10104-10108(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION.
ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G., Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.; "Molecular cloning and nucleotide sequence of CDNA encoding the entire precursor of rat liver medium chain acyl coenzyme A
                        (BI SIMILMAKIII).
NADP (RIBOSE PART) (BY SIMILARITY).
DDA3490FAE28823A CRC64;
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE ACYL-COA DEHYDROGENASE FAMILY.
                                                                                Score 33; DB 1; Length 394;
Pred. No. 30;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001552; Acyl-CoA_dh.
Pfam; PF00441; Acyl-CoA_dh; 1.
Pfam; PF00441; Acyl-CoA_dh; 1.
Pfam; PF02770; Acyl-CoA_dh M; 1.
PROSITE; PS00072; Acyl-CoA_dh M; 1.
PROSITE; PS00073; Acyl-CoA_DH 1; 1.
PROSITE; PS00073; Acyl-CoA_DH 2; 1.
Mitochondrion; Transit peptide.
WITOCHONDRION.
CHAIN 26 421 ACYL-COA_DEHYDROGENASE, MEDII
IRON (HEME PROXIMAL LIGAND)
                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                           421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87280028; PubMed=3611054;
                                                394 AA; 44191 MW;
                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J02791; AAA40670.1; -. PIR; A28436; DERTCM.
                                                                                  61.1%;
                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                           STANDARD;
 82
                                                                                                                                                                                     194 EVTPEGSDY 202
                                                                                                                                                    2 EVVPXGMDY 10
                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P11310; 1EGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: FAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dehydrogenase.";
 82
                                                SEQUENCE
                                                                                                                                                                                                                                                                         ACDM RAT
                                 NP BIND
                                                                                                                                                                                                                                                                                                                                                                                               ACADM.
 METAL
                                                                                                                   Matches
                                                                                                                                                                                                                                         RESULT 15
 SFF
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        FORMS A HYDROGEN-BOND WITH THE FLAVIN N(5) OF THE FAD COFACTOR (BY SIMILARITY). BASE (BY SIMILARITY).
                                                                                        Gaps
                                                                                        .,
0
                                                                Score 33; DB 1; Length 421;
Pred. No. 32;
                                                                                        3; Indels
                                           2CF076F8C919BDE8 CRC64;
                                                                                        2; Mismatches
SPECIFIC.
                                                                                                                                                                      Search completed: June 4, 2003, 13:11:46
Job time: 7.25 secs
                                            46555 MW;
                                                               61.1%;
50.0%;
                                                                                        5; Conservative
                                                                                                               1 EEVVPXGMDY 10
          193
                                                                                                                                   67
                                 401
                                                                                                                            ||::|
EEIIPVAPDY
                                             421 AA;
                                                                            Best Local Similarity
          193
                                ACT SITE
SEQUENCE
                                                                                                                                     28
           ACT_SITE
                                                                  Query Match
                                                                                        Matches
 STATES
                                                                                                               à
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:08:49; Search time 11 Seconds Run on:

(without alignments)
96.134 Million cell updates/sec

1 eevvpxgmdys 11 AUDET-909-3 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

		₩			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1		74.1	156	7	S54619	hypothetical prote
71		70.4	363	7	D69551	pothe
m		66.7	102	N	A42452	V1 protein - tobac
4	36	66.7	341	~	S72649	sucrose-phosphate
Ŋ		66.7	348	~	S72650	sucrose-phosphate
9		66.7	460	7	G96764	unknown protein F2
7		Ġ	1049	7	JC4783	sucrose-phosphate
80		Ġ	1068	-	JQ1329	sucrose-phosphate
თ			1081	~	T09837	sucrose-phosphate
10			1083	7	T04062	sucrose-phosphate
11		ů.	1084	~	T04103	sucrose-phosphate
12			425	~	T24111	hypothetical prote
13		4	433	7	H87660	peptidoglycan-bind
14		64.8	440	~	H72784	probable alkaline
15		4	1150	N	T20173	hypothetical prote
16		•	1474	7	F69009	probable membrane
17		٠.	2747	~	B49132	fat facets (faf) s
18		ω,	66	7	800210	plastocyanin b - L
19		•	S	~	S38255	plastocyanin precu
20	34	ω.	9	~	S58208	
21	34	ë.	O)	7	D98182	O6-methylguanine-D
22	34	ά,	Ċ.	~	AG3104	6-0-methylguanine-
23		θ.	g,	~	F72745	hypothetical prote
24	34		S	-	G69290	probable hexosyltr
25	34	ω.	φ	N	G69350	
56	34	63.0	265	~	E86665	ABC transporter AT
27	34	ë.	9	71	A70164	phenylalanine-tRNA
28	34	٠	œ	73	8113	succinate dehydrog
29	34	63.0	0	7	T48898	disease resistance

disease resistance RND multidang effl	hypothetical prote	hypothetical 367K	partial transposas	hypothetical prote	fibroblast growth	hypothetical prote	hypothetical prote	conserved hypothet	unknown protein [i	transposase ISC105	transposase ISC105	hypothetical prote	pantoate-beta-alan	transposase ISC105
T48899 F83335	T30830	T31308	A99427	A90471	S27021	E90335	S57810	A96001	A96546	F90298	C90307	C64417	G83055	E90487
7 7	10	7	~	~	7	7	7	7	7	7	7	7	~	7
908	1062	3472	97	128	172	184	225	247	257	262	267	276	283	299
63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1
34	34	34	33	33	33	33	33	33	33	33	33	33	33	33

## ALIGNMENTS

1	_
ESULT	
Μ,	S

hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 19-Apr-2002
C;Accession: S54619; S66879

Ride Haan, M.; Maarse, A.C.; Grivell, L.A. submitted to the EMBL Data Library, May 1995 A.Reference number: S54617 A.Accession: S54619

A; Molecule type: DNA A; Residues: 1-156 <DEH>

A;Cross-references: EMBL;X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123 R;de Haan, M.; Grivell, L.A.; Maarse, A.C. submitted to the Protein Sequence Database, July 1996

A;Reference number: S66877 A;Accession: S66879

A;Molecule type: DNA A;Residues: 1.156 cDEW-A;Cress-references: EMBE:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01: A;Experimental source: strain S288C

C; Genetics:

A; Cross-references: SGD:S0005539

A; Map position: 15R

C, Superfamily: hypothetical protein YOR013w

ö Gaps ö 74.1%; Score 40; DB 2; Length 156; 77.8%; Pred. No. 1; Live 1; Mismatches 1; Indels Query Match
Best Local Similarity 77.8'
Matches 7; Conservative

2 EVVPXGMDY 10 ð

50 EVMPLGMDY 58 g

#### RESULT 2

D69551

conserved hypothetical protein AF2411 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

Cyaccesion: D6551

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Richemann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. A; Authores: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.A. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Tille: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

Score 38; DB 2; Length 363; Pred. No. 6.8; 3; Mismatches 2; Indels

Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative

A; Molecule type: DNA

| : | | | : | 120 ENIVPYGIDFS 130

1 EEVVPXGMDYS 11

8 임

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Unknown protein F25F22.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: G96764

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; W. D.; Yu, G.; Fraser, C.C.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719; PMID:11130712
                                                                                                          C;Accession: $72650
Kyomatew, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 222, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate synthas
Kyesference number: $72648; MUID:96439842; PMID:8842155
A;Accession: $72650
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: fruit, cv. Miyagawa-Wase
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-348 <KOM>
A;Cross-references: EMBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060
sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C.Species: Citrus unshiu
C.Date: 24-0ct-1998 #sequence_revision 24-0ct-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE005173; NID: 96692750; PIDN: AAF24856.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 2; Length 348; 66.7%; Pred. No. 17; 1; Indels iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 36; DB
70.0%; Pred. No. 23;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sucrose-phosphate synthase (EC 2.4.1.14) - rice C;Species: Oryza sativa (rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 VIPPGMDFS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEDVPSAMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-460 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: G96764
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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A,Gene: SPS3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JC4783
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A42452

Y. protein - tobacco yellow dwarf virus (strain Australia)

C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72649
R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha
A;Reference number: S72648; MUID:96439842; PMID:8842155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose A; Pathway: sucrose biosynthesis
C; Superfamaily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C; Keywords: glycosyltransferase; haxosyltransferase; sucrose-phosphate synthesis
F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <8585>
       A,Residues: 1-363 «KLE»
A,Cross-references: GB:AE001109, GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265069
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A,Residues: 1-341 <KOM>
A,Cross-references: EMBL:AB006319; NID:g2588891; PIDN:BAA23215.1; PID:g2588892
A,Experimental source: fruit, cv. Miyagawa-Wase
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C,Genetics:
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872649
sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                       Gaps
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66.7%; Score 36; DB 2; Length 102; 60.0%; Pred. No. 4.2;

1; Indels

3; Mismatches

Conservative

. 9

Local Similarity

Query Match

A;Accession: A42452 A;Molecule type: DNA A;Residues: 1-102 <MOR>

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2 EVVPXGMDYS 11

66.7%; Score 36; DB 2; Length 341; conservative 2; Mismatches 1. Thank

Local Similarity

Best Loca Matches

Query Match

A;Gene: SPS2 C;Function:

; 9

|:| ||:| 228 VIPPGMDFS 236

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RESULT 5

3 VVPXGMDYS 11

A;Accession: S72649 A;Status: nucleic acid sequence not shown

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Plant Physiol. 115, 113-121, 1997
A; Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to sugary. A; Recession: T09837
A; Recession: T09837
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1081 < ING-
A; Residues: 1-1081 < ING-
A; Residues: 1-1082 < IND-g2190349; PIDN: CAA72491.1; PID:g2190350
A; Residues: 1-1082 < IND-g2190350
A; Residues: Sp2
C; Molecule type: MRNA
A; Molecule type: MRNA
A; Residues: 1-1081 < ING-
A; Residues: 1-1081 < ING-
A; Residues: 1-1082 < IND-g2190350
A; Residues: 1-1081 < IND-g2190350
A; Residues: Sp2
C; Molecule: Sp2
C; Molecule: Sp2
C; Molecule: Sp3
C
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R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X. submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
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C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: To4103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T. Plant Sci. 112, 207-217, 1995
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; A;Note: P28M11.40
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: cultivar Columbia; BAC clone F28M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T04103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
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A,Cross-references: EMBL:D45890; PIDN:BAA08304.1
A,Experimental source: subsp. Japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-1083 <BEV>
A,Cross-references: EMBL:AL049487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.7
Matches 6; Conservative
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T04103
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C;Accession: JC4783
R;Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella
Gene 170, 217-222, 1996
A;Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
                                                                                                                                                                                                                                                                   A Molecule type: mRNA

A Residues: 1-1049 < VAL>

A; Residues: 1-1049 < VAL>

A; Cross-references: GB:U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270

A; Note: UDPglucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt

C; Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and

C; Genetics:

A; Gene: Sps1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; nucrons: 241; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; 9; Frunction:
A; Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc A; Description: catalyzes the formation of sucrose-6-phosphate synthese; Sucrose-phosphate synthase; sucrose-phosphate synthase; sucrose-phosphate synthase homology C; Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <8SPS>
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C;Species: Craterostigma plantagineum
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%; Score 36; DB 2; Length 1049; 66.7%; Pred. No. 58; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sucrose-phosphate synthase (EC 2.4.1.14) - maize
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les 6; Conservative
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Query Match Matches

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Query Match Best Local &

Matches

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C; Genetics:

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Probable alkaline proteinase APE0263 - Aeropyrum pernix (strain KI)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accesion: H7284
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi Ases G. 83-101, 1999
A;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, T.; Kudoh, Y.; Jin-no, K.; Takahi Ases G. 83-101, 1999
A;Accesion: H2784
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Teference number: A72450; MUID:99310339; PMID:10382966
A;Accesion: H72784
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-440 <KAW>A;Residues: 1-440 <KAW>A;Residues: DDBJ:AP000058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 4, 2003, 13:14:16
Job time : 13 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.8%;
66.7%;
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Matches 6; Conservative
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Matches 6; Conservative
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562 VLPVGIDYS 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: C53A5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                  RESULT 14
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87660
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUD:21173698; PMID:11259647
A;Accession: H87660
A;Status: preliminary
A;Molecule type: DNA
A;Gene: Sps1
A;Map position: 1
A;Map position: 1
A;Introns: 120/3; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
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A;Experimental source: clone R10D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R10D12.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Sacession: T24111 R;Percy, C. Species: Caenorhabditis C;Caenorhabditis C;Caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                            66.7%; Score 36; DB 2; Length 1084; 66.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.8%; Score 35; DB 2; Length 425; 50.0%; Pred. No. 34; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 2; Length 433; Pred. No. 34; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: 219842
A;Accession: T24111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 50.0°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPXGMDYS 11
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A,Gene: CESP:R10D12.10
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A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 656
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A;Accession: T20173
A;Accession: T20173
A;Accession: T20173
A;Accession: proliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1150 <WILL>
A;Cross-references: EMBL:281486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, August 1996
A;Reference number: 219808
A;Accession: T21867
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1150 «WI2>
A;Cross-references: EMBL:278015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decies: 12-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
                                                                                                                                                                   Gaps
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Pred. No. 1e+02;
2; Mismatches 1; Indels
                                                                                             64.8%; Score 35; DB 2; Length 440; 66.7%; Pred. No. 35;
                                                                                                                                                             2; Mismatches
A;Gene: APE0263
C;Superfamily: subtilisin, subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone C53A5
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June 4, 2003, 13:13:35; Search time 14.25 Seconds (without alignments) 79.694 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/Pub. Pub. Pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392085 segs, 103240269 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	Description	Sequence 10, Appl	Sequence 8, Appli	Sequence 4, Appli	Sequence 11, Appl	Sequence 9, Appli	Sequence 27, Appl	Sequence 5111, Ap	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 14, Appl	_	Sequence 10697, A	Sequence 526, App	Sequence 526, App	Sequence 526, App	Sequence 526, App	Sequence 526, App	Sequence 420, App
	ΙD	US-10-217-700-10	US-10-217-700-8	US-10-217-700-4	US-10-217-700-11	US-10-217-700-9	US-09-813-408-27	US-09-815-242-5111	US-10-027-806-4	US-10-034-623-4	US-10-027-801-4	US-09-948-080-14	US-09-738-626-4881	US-09-815-242-10697	US-09-978-295A-526	US-09-978-697-526	US-09-978-192A-526	US-09-999-832A-526	US-09-978-189-526	US-10-174-590-420
	DB	6	σ	σ	0	0	σ	10	o	σ	σ	10	σ	10	σ	σ	6	σ	o,	σ
	Query Match Length DB	1049	1068	1081	1083	1084	440	1062	3472	3472	3472	59	283	299	736	736	736	736	736	736
æ	Query Match	66.7	66.7	66.7	66.7	66.7	64.8	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1
	Score	36	36	36	36	36	35	34	34	34	34	33	33	33	33	33	33	33	33	33
	Result No.		8	ю	4	Ŋ	9	7	80	σ	10		12	13	14	15	16	17	18	19

APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REPERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700

US-10-217-700-8
; Sequence 8, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:

App App App App App App App App App App	APP APP APP APP APP APP APP APP		
	00000000000000	ов: 2	Gaps
Sequence Seq		WITH	Length 1049; 1; Indels 0;
US-10-176-758-420 US-10-175-737-420 US-10-175-737-420 US-10-175-738-420 US-10-175-758-420 US-10-176-482-420 US-10-176-913-420 US-10-176-913-420 US-10-180-552-420 US-10-174-573-420 US-10-174-572-420 US-10-174-572-420	US-10-174-582-420 US-10-175-739-420 US-10-175-740-420 US-10-175-744-420 US-10-176-748-420 US-10-176-748-420 US-10-176-748-420 US-10-176-747-420 US-10-176-747-420 US-10-176-985-420 US-10-176-987-420 US-10-176-987-420 US-10-176-987-420 US-10-176-987-420 US-10-176-987-420 US-10-176-987-420 US-10-176-987-420 US-10-176-987-420 US-10-176-987-420	ALIGNMENTS 17700 FIBER PRODUCING OF SUCROSE PHOSI 710/217,700 2 /394,272	Score 36; DB 9; Pred. No. 96; 2; Mismatches
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7 7 3 8 6 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	736 736 736 736 736 736 736 736 736	ни окниох х но н	vat 11
61.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.		7-700-10 2e 10, Application US, ation No. US2003007012 LINFORMATION: US2003007012 LINFORMATION: Candace CANT: Holaday, A. SCOI OF INVENTION: TRANSGI OF INVENTION: EXPRESE REFERENCE: 201304/100 NT PALLING DATE: 2002- ER APPLICATION NUMBER ER FILING DATE: 1999-( ER APPLICATION NUMBER ER FILING DATE: 1999-( ER APPLICATION NUMBER ER FILING DATE: 1999-( ER APPLICATION NUMBER IN FILING DATE: 1999-( ER PER PALENTING DATE: 1999-( ER PER PER PER PER PER PER PER PER PER PER P	Similarity 6; Conserva vvPXGMDYS 1  :
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	RESULT 1  'Sequence 10, Application US/;  'Bublication No. US2003007019;  'GENERAL INFORMATION:  'APPLICANT: Holaday, A. SCOT;  'TITLE OF INVENTION: TRANSGE;  'TITLE OF INVENTION: TRANSGE;  'TITLE OF INVENTION: TRANSGE;  'TITLE OF INVENTION: EXPRESS;  FILE REFERENCE: 2013-04/1000  'CURRENT FILING DATE: 2002-0;  'EARLIER FILING DATE: 1999-0;  NUMBER: PAPLICATION NUMBER:  EARLIER APPLICATION NUMBER:  EARLIER TINING DATE: 1999-0  NUMBER: PAPLICATION NUMBER:  ENGLIER FILING DATE: 1999-0  SOFTWARE: PALOTION OF: 2.0  SOFTWARE: PATOTION OF: 2.0  SOFTWARE: PATOTION OF: 2.0  SOFTWARE: PATOTION OF: 2.0  CRENIER PATOTION OF: 2.0	cal s cal s 3 3
0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	RESULT 1 US-10-217-' Sequence Publicat. GENERAL APPLICAL APPLICAL TITLE OI TITLE OI TITLE OI TITLE OI TITLE RE CURRENT CURRENT EARLIER EARLIER SOFTWARN SEQ ID N TYPE: TYPE: TYPE:	Query M Best Lo Matches Qy Db

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| Publication No. US20030070191A1
| GENERAL INFORMATION:
| APPLICANT: Haigler, Candace H.
| APPLICANT: Holaday, A. Scott
| TILLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
| TILLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
| TILLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
| TILLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
| FILE REFERENCE: 201344/1000
| CURRENT APPLICATION NUMBER: US/10/217,700
| CURRENT FILING DATE: 1999-09-10
| BARLIER APPLICATION NUMBER: 09/394,272
| EARLIER APPLICATION NUMBER: 09/394,272
| SAFLIER PILING DATE: 1999-09-10
| SOFTWARE OF SEQ ID NOS: 14
| SOFTWARE DE SEC ID NOS: 14
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JAPULCANT: Holaday, A. Scott

TITLE OF INVENTION: EXPRESSINC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSINC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSINC OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT APPLICATION NUMBER: 09/10217,700

CURRENT FILING DATE: 1999-09-10

SARLIER APPLICATION NUMBER: 09/394,272

EARLIER FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 11

LENGTH: 1083

TYPE: PRT

CORGANISM: Arabidopsis thaliana

US-10-217-700-11
                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 9; Length 1068; 66.7%; Pred. No. 98;
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                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Craterostigma plantagineum
US-10-217-700-4
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Sequence 11, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
CURRENT FILING DATE: 2002-08-12
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Best Local Similarity 66.7*
Matches 6; Conservative
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445 VIPPGMDFS 453
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                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Zea mays
US-10-217-700-8
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LENGTH: 1081
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Sequence 27, Application US/09813408

Sequence 27, Application US/09813408

Publication No. US20030049619A1

GENERAL INFORMATION:

APPLICANT: Delagrave, Simon

APPLICANT: Delagrave, Simon

TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial Lik

TITLE OF INVENTION: OF Polynucleotides

TITLE OF INVENTION: OF Polynucleotides

CURRENT APPLICATION NUMBER: US/09/813,408

CURRENT FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 85.
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; Bequence 9, Application US/10217700
; Publication No. US20030070191A1
; GRERRAL INFORMATION:
APPLICANT: Holday, A. SCOCT
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REPERBACE: 201304/1000
; CURRENT APPLICATION NUMBER: US/10/217,700
; CURRENT FILING DATE: 2090-09-10
; BARLIER FILING DATE: 1999-09-10
; SARLIER FILING DATE: 1999-09-10
; SOFTWARE: Patentin Ver. 2.0
; SEP IN O 94
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    66.7%; Score 36; DB 9; Length 1083; 66.7%; Pred. No. 1e+02; 1ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.7%; Score 36; DB 9; Length 1084; Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches 1; Indels
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66.7%; Pred. No. 58;
tive 2; Mismatches 1; Indels
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Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Aeropyrum pernix
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Best Local Similarity 66.73
Conservative 6;
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483 VIPPGMDFS 491
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453 VIPPGMDFS 461
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                                                                                                  3 VVPXGMDYS 11
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ORGANISM: Oryza sativa
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Patent No. US202016047641
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REPERSENCE: DOCRP.002A
CURRENT APPLICATION NUMBER: BALLIER APPLICATION NUMBER: 09/408,020
PRIOR PILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SUFTHARE: FASTSEQ for Windows Version 3.0
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45.5%; Pred. No. 9.1e+02;
Live 4; Mismatches 2; Indels
                                                                                                                                         APPLICANT: Wall, Daniel
APPLICANT: Transck, John D.
APPLICANT: Transck, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, Howard
ITILE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 0/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-12-15
PRIOR FILING DATE: 2001-12-15
PRIOR FILING DATE: 2001-21-6
PRIOR PRIOR PRIOR DATE: 2001-22-16
PRIOR PRIOR DATE: 2001
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Pred. No. 2.4e+02;
0; Mismatches 1;
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ORGANISM: Cenarchaeum symbiosum
                                                                                      Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 85.7%;
Matches 6; Conservative
                         Haselbeck, Robert
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Best Local Similarity 45.5
Matches 5; Conservative
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                                                             Ohlsen, Kari
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US-10-027-806-4
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Sequence 4, Application US/10027801

Publication No. US20030054364A1

GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
ITILE OF INVENTION: UNCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILER REFERENCE: DCORP. 002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 3.0

IENGTH: 3472
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                                                                                               APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR PILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 9.1e+02;
4; Mismatches 2; Indels
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; Sequence 14, Application US/09948080
; Patent No. US20020102702A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER OSTEN, CLAUS
US-10-034-623-4
; Sequence 4, Application US/10034623
; Publication No. US20020198365A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Cenarchaeum symbiosum
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45.5%;
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Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2294 EDVIPRGISFS 2304
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 10; Length 59;
Pred. No. 15;
4; Mismatches 2; Indels
APPLICANT: HALKIER, TORDEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDITZ, PETER
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REPREBENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/09/948,080
CURRENT FILING DATE: 2001-09-06
FRICA REPLICATION NUMBER: US/08/963,851
FRICA REPLICATION DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENITON: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
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; Sequence 4881, Application US/09738626
; Reduction No. US20020197605A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MADO, SEIKO
APPLICANT: TAYASHI, MKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, MKIHIKO
APPLICANT: SENOH, MAKIHIKO
APPLICANT: IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.1%;
Best Local Similarity 45.5%;
Matches 5; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 EXHIPGGLEYS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPXGMDYS 11
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US-09-815-242-10697
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LENGTH: 283
                                                                                                                                                                                                                                                                           SEQ ID NO 14
LENGTH: 59
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Gaps
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Best Local Similarity 40.0%; Pred. No. 94;
Matches 4; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                       APPLICANT: Yamanoto, Robert 1.

APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Derokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-24
PRIOR PELLING DATE: 2000-05-24
PRIOR PELLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-12-26
PRIOR PELLING DATE: 2010-12-16
PRIOR PLING DATE: 2010-12-16
PRIOR PELLING DATE: 2010-12-16
PELLI
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Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                                                                                                    Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
                                  Ohlsen, Kari L.
Zyskind, Judith W.
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Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Napier, Mary A.
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218 EQITPTGIEY 227
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APPLICANT: Haselbeck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-815-242-10697
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APPLICANT:
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| APPLICANT: Streatt, Time..., | APPLICANT: Streatt, Time..., | APPLICANT: Streatt, Time..., | APPLICANT: Streatt, Time..., | APPLICANT: | APPLICANT
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R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/081545
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083554
R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083558 R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081071
R APPLICATION NUMBER: 60/081195
R APPLICATION NUMBER: 60/081195
R FILING DATE: 1998-04-08 R APPLICATION NUMBER: 60/082700
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082797
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082796
R FILING DATE: 1998-04-23
R FILING DATE: 1998-04-23 R FILING DATE: 1998-04-29
RR APPLICATION NUMBER: 60/083495
RFILING DATE: 1998-04-29
RR APPLICATION NUMBER: 60/083496
RFILING DATE: 1998-04-29
RR APPLICATION NUMBER: 60/083499 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09
APPLICATION UNMBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-21 APPLICATION UNDRER: 60/082704 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084640 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29
APPLICATION UNDRER: 60/083742
FILING DATE: 1998-04-30
APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/084414 FILING DATE: 1998-05-06 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084598 PRIOR APPLICATION NUMBER: 60/08441 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-04-15 FILING DATE: 1998-04-22 FILING DATE: 1998-05-06 FILING DATE: 1998-05-07

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CURRENT APPLICATION NUMBER: US/09/978,697 CURRENT FILING DATE: 2001-10-16
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C27
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-03
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR PAPLICATION NUMBER: 60/08550
PRIOR PILING DATE: 1998-05-15
PRIOR PAPLICATION NUMBER: 60/085579
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Patent No. US20020169284A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker Kevin P.
Botstein, David
Desnoyers, Luc
Baton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
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Kuo, Sophia S.
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US-09-978-697-526
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APPLICANT:
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 06/062260
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/077450
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-12
PRIOR PELICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-13
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-21
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-3-3
PRIOR PI
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PRIOR PELLING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081203
PRIOR PELLING DATE: 1998-04-09
PRIOR PELLING DATE: 1998-04-09
PRIOR PELLING DATE: 1998-04-09
PRIOR PELLING DATE: 1998-04-09
PRIOR PELLING DATE: 1998-04-15
PRIOR PELLON NUMBER: 60/081818
PRIOR PELLON NUMBER: 60/081838
PRIOR PELLON NUMBER: 60/081838
PRIOR PELLON NUMBER: 60/082569
PRIOR PELLON NUMBER: 60/082369
PRIOR PELLON NUMBER: 60/08336
PRIOR PELLON NUMBER: 60/08359
PRIOR PELLON NUMBER: 60/08359
PRIOR PELLON NUMBER: 60/08359
PRIOR PELLON DATE: 1998-04-29
PRIOR PELLON DATE: 1998-05-07
PRIOR
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| PRIOR FILING DATE: 1998-05-13
| PRIOR PELING DATE: 1998-05-15
| PRIOR APPLICATION NUMBER: 60/085573
| PRIOR APPLICATION NUMBER: 60/085573
| PRIOR APPLICATION NUMBER: 60/085697
| PRIOR APPLICATION NUMBER: 60/0
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June 4, 2003, 13:09:19; Search time 9.75 Seconds (without alignments) 33.195 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1: /cgn2_6/ptodata/1/iaa/5A COWB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/AA COWB.pep:*

4: /cgn2_6/ptodata/1/iaa/BCOWB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
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                                                                                                                                                                                                                                                                                           262574 segs, 29422922 residues
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the score of the result being printed	O STEATHER TO STEAT

	Description	Sequence 4, Appli Sequence 24, Appli Sequence 11, Appli Sequence 17, Appli Sequence 7, Appli Sequence 7, Appli Sequence 14, Appli Sequence 18, Appli Sequence 8, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 21, Appli Sequence 22, Appli
SUMMARIES	Ç	US-08-853-948B-4 US-08-853-948B-4 US-08-97-367-24 US-08-97-367-24 US-08-718-777-7 US-08-569-147-76 US-08-569-147-76 US-08-569-147-76 US-08-959-147-76 US-08-959-147-76 US-08-969-147-85 US-08-969-147-85 US-08-969-147-85 US-08-865-1144 US-08-865-1144 US-08-86-1147-84 US-08-86-771-77-77-77-77-77-77-77-77-77-77-77-77
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оķо	Query Match	000000mm
	Score	
	No.	1100 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

; TYPE: PRT ; ORGANISM: Citrus unshiu US-08-853-948B-5

Sequence 21, Appl Sequence 6, Appli Sequence 6, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 26, Appli Sequence 19, Appli Sequence 20, Appli	CITRUS AND DNA ENCODING ARG, ASD, Lys, Met, Phe,	gth 341; Indels 0; Gaps 0;	CITRUS AND DNA ENCODING
3 US-08-926-842B-21 2 US-08-464-517-6 3 US-08-464-517-6 1 US-08-246-361A-4 5 PCT-US33-05000-4 5 PCT-US33-05000-4 2 US-08-246-361A-2 2 US-08-246-361A-2 3 US-08-464-317-23 5 PCT-US93-05000-23 1 US-08-464-317-2 1 US-08-472-93 5 US-08-464-517-19 6 US-08-464-517-19 7 US-08-464-517-19 2 US-08-246-361A-20 2 US-08-246-361A-20	ALIGNMENTS  SES3948B  PHOSPHATE SYNTHASE FROM  US/08/853,948B  5-09  Selon 109 is one of Ala  Glu, Gly, His, Ile, Leu  Thr, Trp, Tyr, or Val	Score 36, DB 4; Length Pred. No. 14; 2; Mismatches 1; Inde	ATE SYNTHASE FROM 53,948B
59.3 240 59.3 280 59.3 280 59.3 280 59.3 280 59.3 292 59.3 292 59.3 292 59.3 295 59.3 295 59.3 295 59.3 295 59.3 295	B-4 Application US/08853 6210943 6210943 AKIHAMA, Toyota AKIHAMA, Toyota NVENTION: SUCROSE PHI ENCE: 0049-0235-0 PLICATION NUMBER: US/0 PLICATION NUMBER: US/0 PLICATION NUMBER: US/0 FLICATION NUMBER: US/0 FLICATION: TOS: US/0 FLICATION: TOS: US/0 FLICATION: Xaa at posit REMATION: Yaa at posit FRMATION: Yaa at posit FRMATION: PEO, SET, Th.	66.7% V 66.7% rvative S 11	on US/088 Toyota SUCROSE THE SAME 9-0235-0 UMWBER: U 1997-05 fer. 2.1
28 330 331 332 333 334 335 336 337 337 337 337 337 337 337 337 337	1 1 1 2 2 4 8 8 3 5 3 - 9 4 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4atch 3 5; 3 VVP 228 VIP	1-948B-5 10 Application of Called of Called of Called of Called of Invention of Invention of Invention of Invention of Sec 10 Day of Sec 10 Da
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APPLICANT:
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APPLICANT:
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US-08-718-777-7
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APPLICANT: JEAN; VOBLKER; TONI; GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 36; DB 4; Length 368; 66.7%; Pred. No. 16; tive 2; Mismatches 1; Indels
Query Match 66.7%; Score 36; DB 4; Length 348; Best Local Similarity 66.7%; Pred. No. 15; 1; Indels Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: Emil M.
APPLICANT: Caimi, Perry G.
APPLICANT: Caimi, Perry G.
APPLICANT: Caimi, Perry G.
APPLICANT: Wengy, Zude
APPLICANT: Tarczynski, Mitchell
APPLICANTON NUMBER: US/09/697,367
CURRENT PILING DATE: 1098-MAY-07
PRIOR APPLICATION NUMBER: 60/084,529
PRIOR APPLICATION NUMBER: 60/084,529
PRIOR APPLICATION NUMBER: 1998-MAY-07
PRIOR FILING DATE: 1998-MAY-06
NUMBER: 1998-MAY-06
NUMBER: Mitcrosoft Office 97
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR.1995
CLASSIPICATION 1800
CLASSIPICATION DATA:
APPLICATION NUMBER: US 842,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08429054A Patent No. 5917126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                      Sequence 24, Application US/09697367, Patent No. 6323015, GRNERAL INFORMATION: APPLICANT: Orozco Jr., Emil M. APPLICANT: Caimi, Perry G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 600 THIRD AVENUE
NEW YORK
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Query Match
Best Local Similarity 66.7%
Matches 6; Conservative
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234 VIPPGMDFS 242
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                                                                                                             3 VVPXGMDYS 11
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US-09-697-367-24
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US-08-429-054A-11
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SEQ ID NO 24
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                                                                                                                                                                                                                                  RESULT 3
US-09-697-367-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATH: TILLING DATE: US/08/718,777 FILLING DATE: NOT YET ASSIGNED CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Law Offices of Barbara Rae-Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gervais, M.
TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIONEL DATE Rae-Venter
NAME: BATDATA Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 260 Sheridan Avenue, Suite 440 CITY: Palo Alto STATE: California
                                                           FILING DAIL: 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990
FILING DATE: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
FILING DATE: 20-March-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-July-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08718777; Patent No. 5981852; GENERAL INFORMATION:
                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: CHAILDE A. MUSETIAIN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 661-8000
TELEFAX: (212) 661-8000
TELEFAX: (212) 661-8001
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 328-4477
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Lando, D.
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Voelker, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Unknown MOLECULE TYPE: Peptide US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                                                                                     Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino acid
STRANDEDNESS: Sin
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US-08-569-147-76
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US-08-569-147-82
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APPLICANT: Shewmaker, C. K.

TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STRIEE: California
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                                                                                                                                                  66.7%; Score 36; DB 2; Length 1068; 66.7%; Pred. No. 53; ative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.110.02US
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-0CT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-0CT-1995
PRIOR APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09051341
Patent No. 6124528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415)328-4400
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                                                                                                                                  Query Match
Best Local Similarity 66.7
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Best Local Similarity 66.7
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TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-051-341-7
                                                                                         , MOLECULE TYPE: protein US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                 435 VIPPGMDFS 443
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                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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US-09-051-341-7
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Gaps
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SOFTWARE: Petentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,147

FILING DATE: 25-March-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: TITUJI110, Doreen Yarko

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CARP-0047

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFRAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Score 34; DB 4; Length 140; 75.0%; Pred, No. 13; 75.0%; Artive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
                                                                                                                 TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMANISED ANTIBODIES NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-569-147-76
) Sequence 76, Application US/08569147
) Patent No. 6180377
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 82, Application US/08569147; Patent No. 6120377; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 140 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 WPTGFDY 129
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5 PXGMDYS 11
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Patent No. 5750365;
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 480 West
STREET: Columbus
CITY: Columbus
STATE: Ohlo
STATE: Ohlo
                                                                                                                                                                                                                                                                                                                                                           63.0%; Score 34; DB 4; Length 140; 75.0%; Pred. No. 13; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: WAN DER OSTEN, CLAUS

APPLICANT: HALKIER, TORDEN

APPLICANT: HALKIER, TORDEN

APPLICANT: HALBESEN, CARSTEN

APPLICANT: HANDITS: PETER

APPLICANT: HANDITS: PETER

APPLICANT: HANDITS: PETER

APPLICANT: HANSEN, PETER KAMP

TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS

FILE REFERENCE: 4946,200-US

CURRENT APPLICATION NUMBER: US,08/963,851

CURRENT FILING DATE: 1997-11-04

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 14

SEQ ID NO 14

LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.1%; Score 33; DB 45.5%; Pred. No. 7.5; tive 4; Mismatches
FILING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trulillo, Doreen Yarko
REGISTRATION NUMBER: 35,719
REPERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecalis US-08-963-851-14
                                                                                                                                                                                                                            : 140 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                      TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-82
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                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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UG-08-885-418-8
; Sequence 8, Application US/08885418
; Patent No. 592528
; Patent INPORMATION:
APPLICANT: Chiu, Ing-Ming
; APPLICANT: Poulin, Matthew I.
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
; STREET: $2052 Davis Medical Research Center, 480 West
; STREET: 9th Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                61.1%; Score 33; DB 1; Length 378; 85.7%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/070,165F FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 64;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
TELECOMMUICATION: TELECOMMOICATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                            CLASSIFICATION: 435
CLASSIFICATION: TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acide TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                            : 378 amino acids
amino acid
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 PPGMDYS 145
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: Ohio
RY: USA
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STATE: Oh
COUNTRY:
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Gaps

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Score 32; DB 6; Length 65;
Pred. No. 13;
3; Mismatches 3; Indels
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OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGIGSTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                US-08-580-988A-23
; Sequence 23, Application US/08580988A
; Patent No. 5856161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELBFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
                                               59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     no
DR: internal
                                Ouery Match
Best Local Similarity 45.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 60.0 Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: protein
                                                                                                                               1 EEVVPXGMDYS 11
                                                                                                                                                                      52 KEICPGGMGYT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-580-988A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
              5177197-51
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                                                                                                                                                                                                                                 RESULT 14
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PATENT NO. 517197

PATENT NO. 517197

PAPPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; MERNOTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH, LENA, HELDIN, CARL-HENRIK

LENA, HELDIN, CARL-HENRIK

HUMAN TRANSFORMING GROUNCE STORMAN GROUNCE EXPRESSING

MUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA:

PILING DATE: 27-FEB-1990

SEQ ID NO:51:
                                         RESULT 12
US-09-383-630-6
; Sequence 6, Application US/09383630A
; Patent No. 625532
; Patent No. 625553
; GENERAL INFORMATION:
; APPLICANT: Avner Yayon et al.
; TILE OF INVENTION: FACTOR RECEPTOR ASSOCIATED CHONDRODYSPLASIA
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TRADABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
to an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: Indels
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85.7%; Pred. No. 1.5e+02;
trive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/383,630A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <ur>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: <UNKNOWN>
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFRENCE/POCKET NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562553
                                                                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-383-630-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 85.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                               CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 PPGMDYS 572
139 PPGMDYS 145
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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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audet-909-3.rai

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| Sequence 4, Application US/08460694
| Patent No. S85665
| GENERAL INFORMATION: Andrew TITLE OF INVENTION: PRADI Cyclin and its CDNA NUMBER OF SEQUENCES: A CORRESPONDENCE EXESSIER, COLDSTEIN & FOX P.L.L.C.
| CORRESPONDENCE KESSIER, CRIDGE OF COUNTY OF COUNTY WASHINGTON OF A VOIR Avenue, N.W., Suite 600
| STREET: 1100 New York Avenue, N.W., Suite 600
| STREET: 1100 New York Avenue, N.W., Suite 600
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Search completed: June 4, 2003, 13:14:59 Job time : 9.75 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:04:09; Search time 28.25 Seconds (without alignments) 51.885 Million cell updates/sec

5EQ 47 Title: Perfect score:

COMMON AR.S A. AUDET-909-4 55 1 (eevvpvgmsys 11) Sequence:

908470 segs, 133250620 residues Searched:

BLOSUM62' Gapop 10.0 , Gapext 0.5

Scoring table:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		* Query	* Query			
No.	Score	Match	Length	98	ID	Description
1	50	90.9	11	23	ABB80521	Hepatitis C virus
7	50	90.9	11	23	ABB80522	Hepatitis C virus
м	20	6.06	11	23	ABB80525	•
4	20	6.06	11	23	ABB80526	Hepatitis C virus
Ŋ	20	6.06	11	23	ABB80559	υ
9	20	90.9	11	23	ABB80563	υ
7	20	6.06	11	23	ABB80564	ບ
80	50	90.9	11	23	ABB80565	Hepatitis C virus
9	20	90.9	11	23	ABB80566	U
10	20	90.9	11	23	ABB80567	Hepatitis C virus

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53	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	53	23	20	23	23	23	23	23	23	23			22	
11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	20	11	11	11	11	11	11	7	1022	1022	1022	11
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11	12	13.	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42		44	45

ABB80521 standard; peptide; 11 AA. ABBB05-3Hepartitis C virus NS3/NS4a serine protease inhibitor peptide #1

(first entry)

08-OCT-20g2

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

Synthetic.

/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7" note= "N-terminal acetyl" 11
/note= "C-terminal amide" Location/Qualifiers WO200208251-A2 Key Modified-site Modified-site Modified-site 

31-JAN-2002

19-JUL-2001; 2001WO-US23169.

21-JUL-2000; 2000US-220101P.

(CORV-) CORVAS INT INC.

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Best Local Similarity
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                                                                                                   The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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    residue 7"
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                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                90.9%; Score 50; DB 23; Length 11; 90.9%; Pred. No. 0.0033; ive 0; Mismatches 1; Indels
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         Brunck TK;
                                                                                  Claim 17; Page 64; 69pp; English.
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         Levy OE,
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                           WPI; 2002-361643/39.
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                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketocamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
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Claim 17; Page 64; 69pp; English.
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                                                                     Score 50; DB 23; Length 11;
Pred. No. 0.0033;
0; Mismatches 1; Indels
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                                          Sequence
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Length 11;

DB 23;

90.9%; Score 50;

Query Match

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residue 7"
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Pred. No. 0.0033;
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                                                                                         1 EEVVPXGMSYS 11
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                                                                                   1 EEVVPVGMSYS
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Modified-site
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Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
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Modified-site
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                                              Synthetic
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                             virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                          "Valyl carbonyl forming keto-amide linkage with
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                                                                                                           Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                              Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
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Pred. No. 0.0033;
0; Mismatches 1; Indels
                                                                                                                                                                         'note= "N-terminal acetyl"
                                                                                                                                                                                                             11
/note= "C-terminal amide"
                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                    residue 7"
                                                                                                                                                                                                                                                                                                                             Brunck TK;
                                       ABB80563 standard; peptide; 11 AA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  virus protease
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                                                         ABB80563;
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hopatitis C virus.
                                                                                                                                                                                                                                                                /note= "Leucyl carbonyl forming keto-amide linkage with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease -
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90.9%; Pred. No. 0.0033;
ive 0; Mismatches 1; Indels
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/note= "C-terminal amide"
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       /note= "Norleucyl carbonyl forming keto-amide linkage
with residue 7"
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keto-amide linkage with residue 7"
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                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis {\tt C}
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Pred. No. 0.0033;
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/note= "C-terminal amide"
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/note= "C-terminal amide"
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nes 10; Conservative
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Matches
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Pred. No. 0.0033;
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/note= "C-terminal amide"
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19-JUL-2001; 2001WO-US23169.
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Best Local Similarity 90.9
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                                                                                         The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Alpha-propynyl-glycinyl-carbonyl residue forming a keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
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                                                                                                                                                                                                                                              Score 50; DB 23; Length 11;
Pred. No. 0.0033;
0; Mismatches 1; Indels
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/note= "C-terminal amide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                ABB80568 standard; peptide; 11 AA.
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                                                              Claim 17; Page 65; 69pp; English.
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                 11 AA;
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                                 virus protease
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a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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    residue 7"
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                                                                                                                        Gaps
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                                                                                         90.9%; Score 50; DB 23; Length 11; 90.9%; Pred. No. 0.0033; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-terminal acetyl"
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81.8%;
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                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                          Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have invoide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                   /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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                ABB80529 standard; peptide; 11 AA.
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                                                                                    (first entry)
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ses 9; Conserv
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Matches
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ABB80529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                      Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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Pred. No. 0.02;
0; Mismatches 2; Indels
 2; Indels
 Mismatches
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Best Local Similarity 81.8
Matches 9; Conservative
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 9; Conservative
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31-JAN-2002

Synthetic

ABB80528;

RESULT 13 ABB80528 ö

Gaps

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Sequence

RESULT 14

08-OCT-2002 (first entry)

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                    /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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81.8%; Pred. No. 0.02;
cive 0; Mismatches 2; Indels
                                                                                                                                           'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                              'note= "D-form residue"
                                                                                                                                                                                                                                            /note= "Oxymethionine"
                                                                                                              Location/Qualifiers
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Gaps

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Best Local Similarity 81.8 Matches 9; Conservative

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EEVVPXGMDYS 11

4, 2003, 13:11:13

Search completed: June Job time: 28.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:07:09; Search time 22.5 Seconds Run on:

(without alignments)
100.734 Million cell updates/sec

1 eevvpvgmsys 11 AUDET-909-4 55 Perfect score: Title:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_21:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*

sp\_unclassified:\* sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_virus:\* sp\_human:\* sp\_invertebrate:\* sp\_mammal:\* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp mhc:\* 101

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Q9bha5 plasmodium	Q9bh83 plasmodium	Q971s2 sulfolobus	Q98bp5 rhizobium l	Q8re56 fusobacteri	Q97de7 clostridium	Q8r8k6 thermoanaer	Q8ss39 encephalito	Q9v7c7 drosophila	Q12479 saccharomyc	032330 clostridium	Q9wvw3 mycobacteri	Q96mul homo sapien	Q98fx1 rhizobium 1	QBr126 mus musculu	Q8vd18 mus musculu
. QI	Q9BHA5	Q9BH83	097152	Q98BP5	Q8RE56	Q97DE7	QBRBK6	088839	Q9V7C7	012479	032330	Q9WVW3	Q96MU1	Q98FX1	Q8R126	Q8VD18
DB	10	Ŋ	17	16	16	16	16	'n	S	m	7	N	4	16	11	11
% Query Match Length DB	583	583	219	541	209	84	584	933	1305	156	234	273	290	387	471	484
% Query Match	72.7	72.7	70.9	70.9	69.1	67.3	67.3	67.3	67.3	65.5	65.5	65.5	65.5	65.5	65.5	65.5
Score	40	40	39	39	38	37	37	37	37	36	36	36	36	36	36	36
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### ALIGNMENTS

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Gaps
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                                                                                                                                                                                    SEQUENCE FROM N.A.

Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;

Plasmodium falciparum choline transporter (PfSCT1) gene.";

Submitted (MIG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AY007375; AAG17947.1; -.

EMBL; AY007375; AAG17947.1; -.

InterPro; IPR002123; Acyltransferase.

Pfam; PP01553; Acyltransferase.

SEQUENCE 583 AA; 66917 MW; 2B2BFAE38395E049 CRC64;
                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                   72.7%; Score 40; DB 5; Length 583; 66.7%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                            583 AA.
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les 6; Conservative
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                                                                                                  Choline transporter.
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Q9ВНВЗ;
                                             Q9BHA5;
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Matches
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Probable DNA ligase.
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                                                                                                                                                              NCBI_TaxID=381;
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                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                              SEQUENCE FROM N.A.
Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;
"Plasmodium falciparum choline transporter (PfSCT1) gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodail strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000998; BAB66548.1;
InterPro; IPR004788; RpiA.
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Pfam; PF01553; Acyltransferase; 1.
SEQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;
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Isomerase; Hypothetical protein; Complete proteome.
SEQUENCE 219 AA; 24541 MW; A4E9A3F2C4006D90 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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(TrEMBLrel. 18, Last sequ
(TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                         EMBL; AY007374; AAK14818.1; -. EMBL; AY007373; AAK14817.1; -.
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nes 7; Conservative
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227 IIPVGLSYS 235
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                                                            Plasmodium falciparum.
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Choline transporter.
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Sulfolobus tokođaii
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01-OCT-2001
01-OCT-2001
01-CT-2002
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Bacteriol. 184:2005-2018(2002).

BMBL, AEOIGA32, AAL59465.1; Lipoprotein: Complete proteome. Hypothetical protein. SEQUENCE 209 AA, 24056 MM; E471F6C4911506DA CRC64;
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                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR00997; DNA_ligase.
Pfam, PF01068; DNA_ligase, 1.
PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
PROSITE; PS50160; DNA_LIGASE_A3; 1.
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NCBI_TaxID=76856;
Rhizobium loti (Mesorhizobium loti)
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                                                                                                                                                                                                                                                                                                                    STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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MEDLINE=21886394; PubMed=11889109;
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Matches 7; Conservative
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144 LVPVGISYS 152
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                     MEDLINE=2135935; PubMed=11466286; MEDLINE=2135935; PubMed=11466286; MeDLINE=2135935; PubMed=11466286; MeDLINE=2135935; PubMed=11466286; MoDLINE=2135935; PubMed=11466286; MoDLINE=2135935; PubMed=11466286; MoDLINE=2135935; PubMed=11466286; MoDLINE=2135935; MoDLINE=213595; MoDLINE=2135935; MoDLINE=213595; MoDLINE=213595; MoDLINE=2
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MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
MED (J., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
A complete sequence of T. tengcongensis genome.";
Genome Ress. 12:689-700(2002).
EMBL; ARO1115; AAM22168.1; -
Cell division; Complete proteome.
SEQUENCE 584 AA; 64580 MW; 652BBCC040678F45 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Predicted ATPRAGE of the HSP70 class involved in cell division.
FTSA3 OR TTE1990.
                                                                                                                                                                                  Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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45.5%; Pred. No. 57;
tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 37; DB 16; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein CAC3530.
                          84 AA.
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                          PRT;
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Best Local Similarity 45.55
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 70.0
nes 7; Conservative
                        PRELIMINARY;
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                        297DE7
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Matches
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QBR8K6
Q97DE7
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RESULT 8 088839

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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Adamstides P.G., Sacker B.G., Helt G., Nablson C.R., Miklos G.L.G.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.N.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
Kosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";

Nature 414:450-451(2001).

EMBL, ALS90444; CAD25278.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 933;
                                                                                                                                                                                 Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
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                                                                                                                                                                                                                                                                                                                           Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 933 AA; 106883 MW; CA400EE3A7AFF7CF CRC64;
                                                              01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ATP-dependent RNA helicase (SKI2 subfamily)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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  933 AA.
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                                             Created)
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PRT;
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                                           (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                                      ECU04 0910.
Encephalitozoon cuniculi.
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PRELIMINARY;
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43 EAVVPVGAAYT 53
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les 7; Conserv
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                                           01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Haston M., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,

A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPhorson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPhorson D.,

RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Stden-Kämes I., Simpson M., Stkupski M. P., Smith T.,

She Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Spier E., Spradling A.C., Staplecon M., Strong R., Sun E.,

Sheng Z.-Y., Wassarman D.A., Weinstcock G.M., Weissenbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rh Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CYC2 encodes a factor involved in mitochondrial import of yeast
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Pred. No. 1.4e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003810; AAF58131.1; -.
Flybase; FBGn0034024; CG12961.
SROUENCE 1305 AA; 152870 MW; 8640B93F47B6EF3F CRC64;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
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Mol. Cell. Biol. 13:6442-6451(1993)
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54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 54.5
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STRAIN=FY1679;
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STRAIN=2151;
Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
"Identification of a gene cluster involved in glycopeptidolipid
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
MEDLINE=94169519; PubMed=7764548;

Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;

Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;

"Molecular cloning of a gene, DHS1, which complements a drug-

"Molecular cloning of the yeast Saccharomyces cerevisiae.";

Biosci. Biotechnol. Biochem. 58:391-395(1994).

EMBL; Z74920; CAA99201.1; -.
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MEDILINE=9805381371; PubMed=9393688;
MEDILINE=980538171; PubMed=9393688;
Meath R.J., Goldfine H., Rock C.O.;
"A gene (pisD) from Clostridium butyricum that functionally substitutes for the sn-glycerol-3-phosphate acyltransferase gene (plsB) of Escherichia coli.";
J. Bacteriol. 179:7257-7263(1997).
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                                                                                                                                                                                                                                                                                                        Score 36; DB 3; Length 156;
Pred. No. 21;
2; Mismatches 1; Indels
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SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Acyltransferase; Transferase.
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01-JAN-1998 (TrEMBLrel. 05,
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156 EIIPIGMS 163
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ECKSTAIN-TWO 724;
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ECKSTAIN T.M., Brennan P.J., Inamine J.M., Belisle J.T.;
ECKSTAIN T.M., Brennan P.J., Inamine J.M., Belisle J.T.;
ECKSTAIN TO Graduate Cluster encoding daunorubicin resistance in two strains of Mycobacterium avium serovar 2.";
SUDMILLEG (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF125999; AAD20362.1; -.
EMBL, AF125999; AAD20362.1; -.
Methyltransferase; Transferase.
SEQUENCE 273 AA; 30749 WW; 6543F9C1C5F1B761 CRC64;
biosynthesis and of a gene cluster encoding daunorubicin resistance in two strains of Mycobacterium avium serovar 2."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31891 fis, clone NT2RP7003304, weakly similar to YceA protein
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Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                       Score 36; DB 2; Length 273;
Pred. No. 39;
                                                                                                                                                                                                                                                                                          1; Indels
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"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO56453; BAB71188.1;
InterPro; IPRO1763; Rhodanese-like.
Pfam, PF00581; Rhodanese; 1.
SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last ann
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01-0CT-2001 (TrEMBLrel. 18,
01-0CT-2001 (TrEMBLrel. 18,
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conserv
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SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MRDLINE=21082930; PubMed=11214968;
MRDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
               Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                          Mesorhizobium loti.";
DNA Res. 7:331-338 (2000).
DNA Res. 7:331-338 (2000).
InterPro; IPR002933; Peptidase M20.
Pfam, PF01546; Peptidase M20; I.
Hydrolase; Complete protecome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54.5 kDa protein (Fragment).
Mus musculus (Mouse).
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Job time : 24.5 secs
Rhizobium loti (Mesorhizobium loti).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPVGMSY 10
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                          NCBI_TaxID=381;
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Q8R126;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:08:49; Search time 11 Seconds (without alignments) 96.134 Million cell updates/sec Run on:

1 eevvpvgmsys 11 AUDET-909-4 55 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	° Query Match Length	DB	σı	Description
	38	69.1	1498	5	B97355	DNA segregation AT
7	37	67.3		N	E97333	hypothetical prote
М	36.	65.5		8	S54619	hypothetical prote
4	36	65.5	4	Н	S48515	adenylosuccinate s
2	36			7	A82984	hypothetical prote
9	36			7	AH2679	ATP-dependent DNA
7	36			7	F97461	DNA ligase (AB0425
80	36			7	A72273	hypothetical prote
Q	36			7	A41672	glycerol-3-phospha
10	36			7	T39116 .	probable sulfate p
11	36			7	T40413	sulfate permease -
12	36			~	T31308	hypothetical 367K
13	35			~	E90544	50S ribosomal prot
14	35	•	227	N	E75619	
15	35	•		Н	C42053	
16	35			71	822293	zinc finger protei
17	35	•		7	T16459	hypothetical prote
18	35			7	A34203	DNA-binding protei
19	34	•		~	A42452	
20	34	•		N	H69491	cell division inhi
21	34	•		N	A36893	transcription acti
22	34			N	JC4011	cyclin D2 - rat
23	34	•		2	158372	cyclin D2 - rat
24	34	•		0	A41984	cyclin D2 - mouse
25	34			~	A42822	cyclin D2 - human
	34	•		Ŋ	S57922	D1 -
	34	ä		N	32	D2 -
28	34	61.8		7	JC4579	D2 -
	34	ä		7	S62730	cyclin D1 - zebra

hypothetical protein CAC3530 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001 C;Date: 14-Sep-2001 C;Date: 189-2001 Breton, G;Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A,Reference number: A96900; MUID:21359325; PMID:21359325
A,Accession: E9733
A,Accession: E9733
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-84 <KUR>
A,Rolecule type: Clostridium acetobutylicum ATCC824
C;Genetics: A;Genetics: A;

ó

Gaps ;; 0

Query Match
67.3%; Score 37; DB 2; Length 84;
Best Local Similarity 70.0%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 1; Indels

cyclin D3 - human cyclin D1 - human cyclin D1 - mouse	cyclin D1 - rat hypothetical prote hypothetical prote	hypothetical prote hypothetical prote phosphotransferase	hairy wing suppres hypothetical prote hypothetical prote	ribose 5-phosphate probable membrane probable 3-isoprop hypothetical prote
B42822 A38977 A56523	JC2342 C85432 D71278	T41621 D72253 S46953	S01909 T20173 S57810	F90249 AB0338 A64451 T34536
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292 295 295	295 317 327	521 529 692	944 1150 225	222 240 258 259
61.8 61.8 61.8	61.8 61.8 61.8	61.8 61.8 61.8	61.8 61.8 60.0	60.0 60.0 60.0
6.6.6 . 4.4.4	34 34 34	34 34 44	3 3 4 3 3 4	8 8 8 8 8 8 8 8 8
31 32	33 34 55	36 37 38	39 410	44 44 45 7

## ALIGNMENTS

י אוויסינת
B97355
DNA segregation ATPase, FtsK/SpoiliE family, YUKA B. subtilis ortholog [imported] - Clost
C;Species: Clostrianum acecobitylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: B97355
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Glbson, R.; Lee,
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.K. Barteriol . 183. 4823-4838. 2001
A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A; Reference number: A96900; MUID: 21359325; PMID: 21359325
A;Accession: B97355
A;Status: preliminary
A; Molecule type: DNA
 A;Residues: 1-1498 <kur></kur>
A, Cross-references: GB: AE001437; PIDN: AAK81629.1; PID: g15026814; GSPDB: GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A,Gene: CAC3709
Query Match 69.1%; Score 38; DB 2; Length 1498;
Best Local Similarity 60.0%; Pred. No. 54; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 BEVVPVQMSY 10
1
 RESULT 2

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A,Gene: SGD:ADE12; MIPS:YNL220w
A,Cross-references: SGD:S0005164; MIPS:YNL220w
A,Map position: 14L
C,Super:family: adenylosuccinate synthase
C;Keywords: ligase; purine nucleotide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: circular chromosome
                                                                                                                                                                                     Best Local Similarity 75.0
Matches 6; Conservative
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les 6; Conservative
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                                                                                                                                                                                                                                                                                                               347 IPVGISYS 354
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tes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A82984
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A;Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
A;Experimental source: strain S288C
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A;Molecule type: DNA
A;Residues: 1-433 <DUE>
A;Residues: 1-433 <DUE>
A;Residues: 1-433 <DUE>
A;Cross-references: EMBL:Z71496; NID:g1302236; PIDN:CAA96123.1; PID:g1302237; GSPDB:GNOC
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cross-references: EMBL:L22185; NID:g347862; PIDN:AAA91338.1; PID:g347863
R;Ohanjan, T.; Daignan-Fornier, B.; Krauss, G.
Bubmitted to the EMBL:Data Library, March 1995
A;Reference number: S53085
A;Reference number: S53085
A;Reference number: S53085
A;Rocesion: S53085
A;Rocesion: S53085
A;Rocesion: S63085
A;Rocesion: S73085
A;Rocesion: S73085
A;Residues: 1-433 - COHA>
A;Residues: 1-433 - COHA>
A;Cross-references: EMBL:Z48671; NID:g732938; PIDN:CAA88590.1; PID:g732939
B;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D. A;Reference number: S62944
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                                                                                                                                                                                                     hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein 02612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Date: 08-101-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenylosuccinate synthase (EC 6.3.4.4) - yeast (Saccharomyces cerevisiae) NiAlternate names: protein N1290; protein YNL220w C.Species: Saccharomyces cerevisiae C.Species: Saccharomyces cerevisiae C.Species: Saccharomyces cerevisian 10-Sep-1999 #text_change 16-Jun-2000 C.Accession: S48515; S53085; Š63178 R.Shabes, A.V.; Andreichuk, Y.V.; Holmes, W.M.; Domkin, V.D. Submitted to the EMBL Data Library, July 1993 A.Reference number: S48515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123 R;de Haan, M.; Grivell, L.A.; Maarse, A.C. submitted to the Protein Sequence Database, July 1996 A;Reference number: S6687.
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Pred. No. 12;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                       A,Cross-references: SGD:S0005539
A,Map position: 15R
C,Superfamily: hypothetical protein YOR013w
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Best Local Similarity 66.
                             1 EEVVPVGMSY 10
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EEVINVGVSY 77
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50 EVMPLGMDY 58
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A; Residues: 1-156 < DEH>
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A; Residues: 1-433 <SHA>
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Cjaccession: AH2679
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 24-Aug-2001
C;Accession: Ag298
R;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brisadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004942; GB:AE004091; NID:g9951607; PIDN:AAG08679.1; GSPDB:GN001:
A;Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-dependent DNA ligase Atu0840 [imported] - Agrobacterium tumefaciens (strain C58, Dupc
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number. AB2577; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PA5294 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                              Gaps
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   Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.5%; Score 36; DB 2; Length 541; 60.0%; Pred. No. 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: conserved hypothetical protein H11612
65.5%; Score 36; DB 1; 75.0%; Pred. No. 35; tive 2; Mismatches
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A; Title: Transcriptional regulation of p90 with sequence homology to Escherichia coli gl;
A; Reference number: A41672; MUID:92084678; PMID:1721057
A; Accession: A41672
A; Molecule type: mRNA
A; Residues: 1-827 < SHI>>
A; Cross-references: GB:M77003; NID:g193366; PIDN:AAA37647.1; PID:g193367
A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1.840 <HUN>
A;Cross-references: EMBL:AL132779; PIDN:CABG0015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A;Experimental source: strain 972h-; cosmid c869
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A;Experimental source: strain 972h-; cosmid c3H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39116
R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 840;
Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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A;Status: prealiminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-877 <LYN>
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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                                                                                                                                                                                                           DB 72;
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                                                                                                                                                                                                                      Score 36;
Pred. No.
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Local Similarity 77.8%;
les 7; Conservative
                                                                                                                                                                                                                         65.5%;
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z21926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VVPVGMSYS 11
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349 VIPVGISY 356
                                                                                                                                                                                                                                                                                                                                 3 VVPVGMSY 10
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Best Local Similarity
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A;Gene: SPDB:SPAC869.05c
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Matches
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                                                                                                                                                                                                                DNA ligase (AB042527) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C; Species: Agrobacterium tumefaciens
C; Dates: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession: F99461
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R; Goodner, B.; Hinkle, G.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
A; Reference number: A97359; PMID:11743194
A; Residues: 1-573 < KKR>
A; Residues: 1-573 < KKR>
A; Residues: 1-573 < KKR>
A; Cometics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUD:99287316; PMID:10360571
A;Accession: A72273
A;Status: preliminary
A;Molecule type: DNA
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A,Cross-references: GB:AE001783; GB:AE000512; NID:g4981832; PIDN:AAD36352.1; PID:g498183
A,Experimental source: strain MSB8
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72273
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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hypothetical protein TM1277 - Thermotoga maritima (strain MSB8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.5%; Score 36; DB 2; Length 573; 60.0%; Pred. No. 48; tive 3; Mismatches 1; Indels
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                       442 EQLVPVGKAY 451
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                                       1 EEVVPVGMSY 10
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A41672
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274 DQVVPVGLS 282
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                        C;Species: Cenarchaeum symbiosum
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T31308
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
J. Bacteriol. 180, 5003-5009, 1998
A;Title: Genomic analysis reveals chromosomal variation in natural populations of the un A;Reference number: Z20994; MUID:98422450; PMID:9748430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50S ribosomal protein 120 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Accession: E90544
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
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(Species: Deinococcus radiodurans
(Species: Deinococcus radiodurans
(Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
(SACcession: B75619
(R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
(M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
(S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
(Science 286, 1571-1577, 1999
(A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
(A) **Reference number: A75250; MUID:20036896; PMID:10567266
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                                                                                                                                                                                                                                                                                                                   A;Residues: 1-3472 <SCH>
A;Cross-references: EMBL:AF083072; NID:g3599393; PID:g3599394; PIDN:AAC62699.1
C;Superfamily: Cenarchaeum symbiosum hypothetical 367K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
hypothetical 367K protein - Cenarchaeum symbiosum
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54.5%;
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2294 EDVIPRGISFS 2304
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Matches 7; Conservative
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A, Residues: 1-227 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Genetic code: SGC3
                                                                                                                                                                                                                                       A; Accession: T31308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: E75619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: MYPU 2610
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C,Accession: C42053
R;Haefliger, J.A.; Bruzzone, R.; Jonkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Paul, D.L.
Biol. Chem. 267, 2057-2064, 1920
A;Hitle: Four novel members of the connexin family of gap junction proteins. Molecular cl
A;Reference number: A42053; MUID:92112940; PMID:1370487
                                                           A; Gene: DRB0013
A; Map position: megaplasmid
A; Genome: plasmid
A; Note: plasmid
A; Note: plasmid MP1
C; Superfamily: Deinococcus radiodurans megaplasmid hypothetical protein DRB0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap junction protein Cx33 - rat
N,Alternate names: connexin 33
C,Species: Rattus norvegicus (Norway rat)
C,Species: Q4-Mar-1993 #sequence_revision 02-Jun-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;COSB-references: GB:M76534; NID:g203663; PIDN:AAA40998.1; PID:g203664
A;NOte: sequence extracted from NCBI backbone (NCBIP:76095)
C;Superfamily: gap junction protein transmembrane protein
C;Keywords: gap junction; phosphoprotein; transmembrane protein
F;1-23/Domain: intracellular #status predicted <INT1>
F;24-1/Domain: extracellular #status predicted <IM1>
F;24-7/Domain: extracellular #status predicted <IM2>
F;78-97/Domain: extracellular #status predicted <IM2>
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                                                                                                                                                                                                                                                                           63.6%; Score 35; DB 2; Length 227; 54.5%; Pred. No. 28; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 1; Length 286;
Pred. No. 36;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;208-234/Domain: transmembrane #status predicted <TM4> F;235-286/Domain: intracellular #status predicted <INT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;151-187/Domain: transmembrane #status predicted <TM3>F;188-207/Domain: extracellular #status predicted <EE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;98-150/Domain: intracellular #status predicted <INT2>
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A; Experimental source: strain R1
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Matches 6; Conservative
                                                                                                                                                                                                                                                                              Query Match 63.6
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPVGMSYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 ESVLPIGHSFS 53
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audet-909-4.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 4, 2003, 13:04:34; Search time 6.25 Seconds (without alignments) 72.998 Million cell updates/sec Run on:

AUDET-909-4 55

1 eevvpvgmsys 11 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table: 'BLOSUM62

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1	P80210 saccharomyc	Q9htr0 pseudomonas	Q61586 mus musculu	564		Q8rg86 fusobacteri	_						Q04827 rattus norv		_		xenopn	gallus	xenopu	gallus	l homo		mus n	m		0		Q01606 klebsiella	0	2 esche	1310 homo sap	P41367 sus scrofa
SUMMARIES	ID	A	PURA_YEAST	NOM2 PSEAE	PLSB_MOUSE	PLSB_RAT	SULH SCHPO	CARB FUSIN	RL20_MYCPU	CXA6_RAT	PLSB HUMAN	ZEP1 HUMAN	Y11K TYDVA	POBR_ACICA	CGD2 RAT	CGD2_HUMAN	CGD2 MOUSE	CGD1_BRARE	CGD1 XENLA	CGD2 CHICK	CGD2 XENLA	CGD1 CHICK	CGD3 HUMAN	CGD1 HUMAN	CGD1_MOUSE	CGD1 RAT	OAT6_HUMAN	SUHW DROME	YC10 METJA	PHOE KLEOX	PHOE_ENTCL			ACDM_PIG
	DB	н	-	Н	H	Н	Н	Н	Н	Н	•	-	• •		Н	Н	Н	н	Н	Н	Н	Н	٦	Н	-	Н	Н	ч	Н	Н	Н	Н	П.	7
	Length	1498	432	488	827	828	877	1058	116	286	828	2717	102	271	288	289	289	291	291	291	291	292	292	295	295	295	691	944	258	349	350	2	421	421
		1.6	٠	5.5	5.5	ī.	.5	.5	9.	9.6	9.	9.6	8.	8.1	•	٠				٠	1.8	•	٠	•	•	•	•	•	0.0	•	٠		0.0	0.
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	Result No.	-	7	Э	4	ហ	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q9krb0 vibrio chol Q9nzm5 homo sapien P45021 haemophilus Q15067 homo sapien Q921n0 cavia porce Q921n0 cavia porce Q9200 mus musculu P07872 rattus norv P46720 rattus norv P46720 rattus norv P46720 accharomyc P32784 saccharomyc P32784 saccharomyc O67287 aquifex aeo	
AROA VIBCH GSR2_HUMAN GYOA_HABIN CAOI_CAVPO CAOI_CAVPO CAOI_RAT OAIP_RAT OAIP_RAT SYIC_RASI SYIC_YBASI SCTI_YBASI WUS2_AQUAE	
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4426 6610 6610 6611 6611 7334 7620	
W W W W W W A A A A A A A A A A A A A A	

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"Sequence and molecular characterization of a DNA region encoding a "Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clostridium acetobutylicum.";
J. Bacteriol. 175:3394-3400(1993).
-!- SIMILARITY: BELONGS TO THE FTSK/SPOIIIE FAMILY.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 76 and 106.
                                                                                                                                                                                                                                                      STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriul. 183:4823-4838 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.1%; Score 38; DB 1; Length 1498; 60.0%; Pred. No. 21; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP BIND 675 682 ATP (POTENTIAL).
SEQUENCE 1498 AA, 168968 MW, FF42037A335A9649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE007866; AAK81629.1; -.
EMBL; X65276; CAA46379.1; ALT FRAME.
InterPro; IPR002543; FtsK SpoIIIE.
Pfam: PF01580; FtsK SpoIIIE; 2.
Pfam: PF01580; FtsK SpoIIIE; 2.
Hypothetical protein; ATP-binding; Complete proteome.
NP_BIND 675 ARP (POTENTIAL).
                                   (Rel. 28, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
PRT; 1498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
                                                                                         Hypothetical protein CAC3709.
CAC3709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
STANDARD;
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Matches 6; Conserva
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=1488;
                                       01-FEB-1994
                                                            16-OCT-2001
Y1A9 CLOAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93388587, PubMed=8376380;
MEDLINE=93388587, PubMed=8376380;
Seidler R., Hobert O., Johannes L., Faulhammer H., Krauss G.,
"Characterization of two novel single-stranded DNA-specific
autonomously replicating sequence-binding proteins from Saccharomyces cerevisiae, one of which is adenylosuccinate synthetase.";
J. Biol. Chem. 268:20191-20197(1993).
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NOVO PATHWAY OF PURINE NUCLEOTIDE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: AMP biosynthesis; first committed step.
                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
D - G (IN REF. 4).
W, FFEEB44F46349570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moestl D.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            Shabes A.V., Andreichuk Y.V., Holmes W.M., Domkin V.D., Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                            Ohanjan T., Daignan-Fornier B., Krauss G.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                    432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probon; PD001188; Asuc synthase; 1.
TIGRFAMS; TIGR00184; purh; 1.
PROSITE; PS00513; ADENYLOSUCCIN SYN 2; 1.
PROSITE; PS01566; ADENYLOSUCCIN SYN 1; 1.
Purine biosynthesis; Ligase; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD; S0005164; ADE12.
InterPro; IPR001114; Asucc_synthtase.
Pfam; PF00709; Adenylsucc_synt; 1.
                                                                                                                                                    01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48148 MW;
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                                                                                                                                                                                                                                      ADE12 OR YNL220W OR N1290.
                 1276 EQKIPMGMSY 1285
                                                                                                                    STANDARD;
1 EEVVPVGMSY 10
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144
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236
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236
432 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                        (AMPSase)
                                                                                                                    PURA YEAST
P80210;
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ACT_SITE
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINE-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
Strover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TICRFAMs, TICR00797, matE; 1.
Transport, Antiport, Sodium transport, Transmembrane, Inner membrane;
                              Gaps
                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
Probable multidrug resistance protein norM 2 (Na(+)/drug antiporter)
(Multidrug-efflux transporter)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential).
-!- SIMILARITY: BELONGS TO THE MULTI ANTIMICROBIAL EXTRUSION (MATE)
FAMILY. NORM (TC 2.A.66.1.1) SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i - FUNCTION: FUNCTIONS AS A NA(+)/DRUG ANTIPORTER (BY SIMILARITY)
                              ;
                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
65.5%; Score 36; DB 1; Length 432; 75.0%; Pred. No. 15;
                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8202CBB392C0F9FD CRC64;
                              2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002528; MatE. Pfam; PF01554; UPF0013; 2.
              Local Similarity 75.0 hes 6; Conservative
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:959-964 (2000)
                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
                                                                                      346 IPVGISYS 353
                                                          4 VPVGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=287;
                                                                                                                                                                 NOM2 PSEAE
Q9HTRO;
                                                                                                                                                                                                                                                                                                                       Pseudomonas
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Length 488;

DB 1;

Score 36;

65.5%;

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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                  Shin D.-H., Paulauskis J.D., Moustaid N., Sul H.S.,

"Transcriptional regulation of p90 with sequence homology to
Escherichia coli glycerol-3-phosphate acyltransferase.";

-! CATALYTIC ACTIVITY: Acyl-CoA + sn-glycerol 3-phosphate = COA + 1-
acyl-anglycerol 3-phosphate.

-! PATHWAY: FIRST STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS. IT MAY
ALSO FUNCTION IN THE REGULATION OF MEMBRANE BIOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial outer membrane (By similarity).
-!- TISSUE SPECIFICITY: HIGHEST LEVELS LIVER, INTERMEDIATE LEVELS IN MUSCLE AND KIDNEY, AND LOWEST LEVELS IN LUNG AND BRAIN.
-!- SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.
MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                               PLSB_MOUSE STANDARD; PRT; 827 AA.
061586;
01-NS6;
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycerol-3-phosphate acyltransferase, mitochondrial precursor (EC 2.3.1.15) (GPAT) (PP0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:109162; Gpam.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
Transmembrane; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A64EDE697BD664B3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                3; Mismatches
 Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92084678; PubMed=1721057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93689 MW;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M77003; AAA37647.1; -.
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                6; Conservative
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471
494
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286 MVPVGLSYA 294
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349 VIPVGISY 356
                                            3 VVPVGMSYS 11
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                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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575
594
827 AA;
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Best Local Similarity
Matches 6; Conserv
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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DOMAIN
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                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TOPOLOGY.
STRAIN=Spraque-Dawley; TISSUE=Liver;
MEDLINE=20493538; PubMed=10924502;
Balija V.S., Chakraborty T.R., Nikonov A.V., Morimoto T., Haldar D.;
"Identification of two transmembrane regions and a cytosolic domain of
rat mitochondrial glycerophosphare acyltransferase.";
J. Biol. Chem. 275:31668-31673(2000).
-I. CATALYTIC ACTIVITY: Acyl-CoA + sn-glycerol 3-phosphate = COA + 1-
                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Mitochondrion; Transit peptide.
TRANSIT
1 ? MITOCHONDRION (FOTENTIAL).
GLYCERGL-3-PHOSPHATE ACYLTRANSFERASE.
DOMAIN ? 471 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99376617; PubMed=10446428;
Bhat B.G., Wang P., Kim J.-H., Black T.M., Lewin T.M.,
Fiedorek F.T. Jr., Coleman R.A.;
"Rat sn-glycerol-3-phosphate acyltransferase: molecular cloning and
characterization of the CDNA and expressed protein.";
Biochim. Biophys. Acta 1439:415-423(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSO FUNCTION IN THE REGULATION OF MEMBRANE BIOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                  199564, P97566; P97565; 035349; 01-NOV-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-UUL-1999 (Rel. 37, Last sequence update) 63, Last annotation update) 63, Last annotation update) 62, 2.3.1.15) (GPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 828;
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InterPro, IPR002123; Acyltransferase.
Bfam; PF01553; Acyltransferase; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C -> F (IN REF 2).
S -> P (IN REF 2).
L -> V (IN REF 2).
IL-> V (IN REF 2).
ILF -> NLL (IN REF 2).
R -> W (IN REF 2).
SAGGL -> LEPEP (IN REF 2).
G -> H (IN REF 2).
G -> A (IN REF 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
828 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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Pred. No.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ACTIVITY.
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STANDARD;
                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
-!- SIMILARITY: CONTAINS 1 STAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                                 877 AA
                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
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                             349 VIPVGISY 356
3 VVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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074377;
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STRAIN-ATCC 2586;

MEDLINE=21886394; PubMed=11889109;

REDLINE=21886394; PubMed=11889109;

REDLINE=21886394; PubMed=11889109;

REDLINE=21886394; PubMed=11889109;

Battacharyya A., Battana A., Cardner W., Grechkin G., Zhu L.,

Battacharyya A., Battan A., Chaga O., Goltsman E., Earnal A.,

Larsen N., D'Souza M., Walunas T., Puech G., Hamelkorn R.,

Larsen N., Coverbeck R.,

"Genome sequence and analysis of the oral bacterium Pusobacterium
nuclearum strain ATCC 2586";

"Genome sequence and analysis of the oral bacterium Pusobacterium
nuclearum strain ATCC 2586";

"J. Bacteriol. 184:2005-2018(2002).

-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

Dhosphate + L-glutamate + carbamoyl phosphate.

-!- PATHWAY: Arginidine biosynthesis.

-!- PATHWAY: Arginidine biosynthesis, first step.

-!- PATHWAY: Pyrimidine biosynthesis; first step.

-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain

promotes the hydrolysis of glutamine to ammonia, which is used by

--- CALTALYTIC (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                     65.5%; Score 36; DB 1; Length 877; 77.8%; Pred. No. 31; tive 1; Mismatches 1; Indels
                                                                                                                                                                                            56995A8493371E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           PRT; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SIMILARITY: BELONGS TO THE CARB FAMILY.
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tes 7; Conserv
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ID CARB_FUSNN
AC Q8RGB6;
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EMBL; AE010554; AAL94625.1; ALT\_INIT. InterPro; IPR005483, CRase L. InterPro; IPR005479; Crase L. InterPro; IPR005480; CPase L\_D3.

Pfam; PF00916; Sulfate\_transp; 1.
Pfam; PF01740; STAS; 1.
TIGRAMS; TIGRO0815; SulP; 1.
PROSITE; PS01130; SLC26A; 1.
PROSITE; PS50801; STAS; 1.

Transport; Transmembrane.

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RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";

Nucleic Acids Res. 29:2145-2153 (2001).

Nucleic Acids Res. 29:2145-2153 (2001).

-i. FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS OF THAT SUBUNIT (BY SIMILARITY).

-i. SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                           OLIGOMERIZATION DOMAIN.
CARBANOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
InterPro; IPR005481; CPase L N.

InterPro; IPR004362; MGS_like.
Pfam; PF002089; CPSase_L_Chain; 2.
Pfam; PF027087; CPSase_L_D2; 2.
Pfam; PF027087; CPSase_L_D3; 1.
Pfam; PF021047; MGS, 1.
PROSITE; PR00086; CPSASE_1; 2.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosowal protein L20.
Mycoplasma pulmonis.
Bacteria: Firmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 1058;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117451 MW; ED7037AF77C1E39F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL445563; CAC13434.1; -. MypuList; MYPU_2610; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|| |::||
190 EIVPNGLNYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                         546
929
1058
546
1058
210
352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
RL20 MYCPU
ID RL20 MYCPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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DOMAIN
REPEAT
REPEAT
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q98QV0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
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                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                           ..
0
                                                                                                               Score 35; DB 1; Length 116;
Pred. No. 6.1;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
         Pfam, PF00453; Ribosomal L20; I.
PRINTS, PR0062; RIBOSOMALL20.
PRODOM, PD002389; RIBOSOMALL20.
TIGREAM; TIGR01032; rplT bact; 1.
PROSITE; PS00937; RIBOSOMALL20; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
SEQUENCE 116 AA; 13565 MW; C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gap junction alpha-6 protein (Connexin 33) (Cx33).
                                                                                                                                                                                                                                                             PRT; 286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M76534; AAA40998.1; -.
PIR; C42053; C42053.
InterPro; IPR000500; Connexin.
Pfam; PF00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SWART; SM00037; CNX; 1.
PROSITE; PS00409; CONNEXINS 1; 1.
PROSITE; PS00409; CONNEXINS 1; 1.
InterPro; IPR001081; Ribosomal_L20.
                                                                                                                 Query Match 63.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gap junction; Transmembrane.

1 20
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
41
76
163
184
208
                                                                                                                                                                      3 VVPVGMSYS 11
                                                                                                                                                                                             68 VRPLGMSYS 76
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
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TRANSMEM
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DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                               CXA6 RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:273-281(2000)
--- CATALYTIC ACTIVITY: ACY1-CAA + sn-glycerol 3-phosphate = COA + 1-acy1-sn-glycerol 3-phosphate.
--- PATHWAY: FIRST STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS. IT MAY ALSO FUNCTION IN THE REGULATION OF MEMBRANE BIOGENESIS.
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MINIO VOLSONO.

ThreePro; IPRO00123; Acyltransferase.

Pfam; PF01553; Acyltransferase; 1.

Phospholipid biosynthesis; Transferase; Acyltransferase;

Transmembrane; Mitochondrion; Transit peptide.

TRANSIT 1 2 MITOCHONDRION (POTENTIAL).

CHAIN 7 828 GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.

DOMAIN 7 471 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRIAL INTERMEMBRANE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial outer membrane (By similarity).
SIMILARITY: BELONGS TO THE GPAT / DAPAT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                          ö
                                                                                                                                                                                                                                                                09HCI2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
61yeerol-3-phosphate acyltransferase, mitochondrial precursor
(EC 2.3.1.15) (GPAT).
                                              Score 35; DB 1; Length 286; Pred. No. 15; 0; Indels 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashwell R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
286 CYTOPLASMIC (POTENTIAL).
32860 MW; A585266ACA2ACCF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93836 MW; E5CD321A23D0B65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                     828 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL391986; -; NOT ANNOTATED CDS.
EMBL; AB046780; BAB13386.1; -.
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 167-828 FROM N.A.
                                                    63.68;
                                                                   66.78;
                                                                     Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                              ::|||||:|
274 DQVVPVGLS 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471
494
574
                                                                                                                         1 EEVVPVGMS 9
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                  286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495
575
594
828 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             GPAM OR KIAA1560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                     PLSB HUMAN
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                RESULT 10
PLSB_HUMAN
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DB 1; Length 828;

Score 35; DB Pred. No. 46;

63.6%;

Best Local Similarity

Query Match

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Biochemistry 31:3907-3917(1992).

-!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIVY. IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEUKIN-2 RECEPTOR, AND INTERPERON-BETA GENES. IT MAY ACT
                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
2inc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-EP) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Blochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: BY MITOGEN AND PHORBOL ESTER.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fan C.M., Maniatis T.; "A Maniatis T.; "A DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence."; Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92232684; PubMed=1567844;
Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
ö
  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91064333; PubMed-2248949;
Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
Gronenborn A.M.;
                                                                                                                                                                            2717 AA.
3; Mismatches
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-90169514; PubMed=2106471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 2087-2142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 2113-2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X51435; CAA35798.1; -. PIR, A34203; A34203. PDB; 3ZNF; 15-JAN-92. PDB; 4ZNF; 15-JAN-92. PDB; 1BBO; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-CELL ACTIVATION.
5; Conservative
                                                                                                                                                                            STANDARD;
                                                                           349 IIPVGISY 356
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                      3 VVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gronenborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      HIVEPI OR ZNF40.
                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                        PRDII-BF1)
                                                                                                                                                                                ZEP1 HU
P15822;
                                                                                                                                                         ZEP1 HUMAN
  Matches
                                                                                                                                     RESULT 11
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L05770; AAC37162.1; ...
InterPro; IPR000285; HTH_IC1R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter calcoaceticus.
                    Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
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                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 EVVPVARSY 134
                                                                                                2 EVVPVGMSYS 11
                                                                                                                                   7 QVVPSGINYS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BD413 / ADP1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                 Acinetobacter.
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DNA BIND
                                                                                                                                                                                                                                    POBR ACICA
Q43992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                               RESULT 13
POBR_ACICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
CGD2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINES-21885538, PubMed=1546458;

Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component of thobacco pallow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";

Virology 187:642(1992).
                                                 InterPro; IPR000822; Znf C2H2.
Pfam; PF00096; zf-C2H2; 5.
SMRNTS; PR00048; ZINCFINGER.
SMART; SM00355; ZnF C2H2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS00027; ZINC_FINGER_C2H2_1; 4.
Transcription regulation; Zinc_finger; Metal-binding; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%; Score 35; DB 1; Length 2717;
66.7%; Pred. No. 1.6e+02;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297217 MW; D45D3CA951FEA561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                         POLY-SER.
C2HC-TYPE (POTENTIAL).
ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OT-1993 (Rel. 27, Last annotation update)
Hypochetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 102 AA.
                                                                                                                                                                                                                    ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A42452; A42452.
InterPro; IPR002621; Gemini mov. Jefan; PP01708; Gemini mov; J. Hypothetical protein.
SEQUENCE 102 AA; 11178 MW; A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M81103; AAA47947.1; -.
TRANSFAC; T00497; -.
Genew; HGNC:4920; HIVEP1.
MIM; 194540; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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2109
2139
2088
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2095
2108
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ZN FING
ZN FING
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DOMAIN
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ZN_FING
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Y11K TYDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                          HELIX
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Dimarco A.A., Averhoff B.A., Ornston L.N.;

Genetification of its role in the expression of pobA, the structural gene for p-hydroxybenzoate hydroxylase in Acinetobacter

Galoaceticus. ";

J. Bacteriol. 175:4499-4506 (1993).

-!- FUNCTION: POSITIVE REGULATOR OF THE POBA GENE FOR P-

HYDROXYBENZOATE HYDROXYLASE.

-!- INDUCTION: BY P-HYDROXYLASE.

-!- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                      Gaps
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61 61 R->H: IN ADP249; LOSS OF ACTIVITY.
271 AA; 30764 MW; 40B7DA8531389084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.8%; Score 34; DB 1; Length 271; 77.8%; Pred. No. 23;
61.8%; Score 34; DB 1; Length 102; 60.0%; Pred. No. 8.5;
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                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          [5-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P-hydroxybenzoate hydroxylase transcriptional activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 AA.
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                                                                  3; Mismatches
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Query Match
Best Local Similarity
 NCBI_TaxID=9606;
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                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=55011623; PubMed=7926809;
HOBOKAWA Y., Onga T., Nakashima K.;
Hodokawa Y., Onga T., Nakashima K.;
HINDUCTION of D. and D3 cyclin-encoding genes during promotion of the G1/S transition by prolactin in rat ND2 cells.";
Gene 147:249-222(1994).
-!- FUNCTION: BSSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S (START) TRANSITION.
                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERLELYHEROWINE KINASE HOLORENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene. CONFLICT 68 68 E -> G (TN PRP 2)
                                                                                                                     MEDLINE=93275661; PubMed=8502486;
Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
Francke U., Jolicoeur P.;
"The Vin-1 gene, identified by provirus insertional mutagenesis, is
the cyclin D2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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104 104 C -> V (IN REF. 2).
232 232 T -> A (IN REF. 2).
288 AA, 32826 MW, 4B522BF4E9835FC1 CRC64;
           16-OCT-2001 (Rel. 40, Last annotation update)
G1/S-specific cyclin D2 (Vin-1 proto-oncogene).
CGND2 OR VIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGD2_HUMAN STANDARD; PRT; 289 AA. P30279; Q13955; 01-APR-1993 (Rel. 25, Created) 15-JAPR-1993 (Rel. 25, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) G1/S-specific cyclin D2.
01-OCT-1993 (Rel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin, C; 1.
SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L09752; AAA41010.1; -. EMBL; D16308; BAA03815.1; -.
                                                                                                                                                                                      Oncogene 8:1661-1666(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EEVVPVGMSY 10
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                                                                                                           SEQUENCE FROM N.A.
                                                                                  NCBI_TaxID=10116;
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OCCUPATION
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-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (START) TRANSITION.
-!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLDENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

BEDLINE-23265844, PubMed=8455931;
Palmero I., Peters G.;
Palmero I., Jolder A., Sinclair A.J., Dickson C., Peters G.;
"Cyclins D1 and D2 are differentially expressed in human B-lymphoid
SEQUENCE FROM N.A.
MEDLINE=92347451; PubMed=1386336;
Xiong Y., Menninger J., Beach D., Ward D.C.;
"Molecular cloning and chromosomal mapping of CCND genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92347850; PubMed=1386335;
Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.8%; Score 34; DB 1; Length 289; 60.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyajima N.;
Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF02984; cyclin; 1.

SMART; SM00385; CYCLIN; 1.

Cyclin; Call cycle; Cell division; Multigene family.

Cyclin; Call cycle; Cell division; Multigene family.

CONFLICT 166 167 KL -> NV (IN REF. 5).

CONFLICT 224 Z24 T -> H (IN REF. 5).

SEQUENCE 289 AA; 33067 WW; B4E5FEF476D76D90 CRC64;
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EMBL; X68452; CAA48493.1; --
EMBL; D13629; BAA020802.1; --
EMBL; M80083; AAA109588.1; --
EMBL; M880083; AAA51928.1; --
EMBL; M880081; AAA51928.1; --
EMBL; M880081; AAA51928.1; JOINED.
EMBL; M880081; AAA51928.1; JOINED.
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InterPro; IPR004367; Cyclin Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene 8:1049-1054(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-240 FROM N.A.
                                                                                                                                                      human D-type cyclins.";
Genomics 13:575-584(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:1583; CCND2.
MIM; 123833; -.
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PIR; S26580; S26580.
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Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 cell lines.
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0; Gaps 2; Mismatches 2; Indels Matches 6; Conservative

0;

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Search completed: June 4, 2003, 13:11:47 Job time: 7.25 secs

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Sequence 111, App
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Sequence 2, Appli
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79.694 Million cell updates/sec
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| cgn2_6/ptodata2/2/pubpaa/PCT_NEW_PUB.pep:*
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| cgn2_6/ptodata2/2/pubpaa/NEOS_PUBCOMB.pep:*
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                                                                                                                   June 4, 2003, 13:13:35 ; Search time 14.25 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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858 77648 - PU 25 6 P	Sequence 356, App Sequence 236, App Sequence 1245, App Sequence 234, App
	US-10-153-668-356 US-10-153-668-236 US-09-764-864-1245 US-10-153-668-234
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## ALIGNMENTS

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Sequence 4, Application US/10027806
| Patent No. US20020160476A1
| GENERAL INFORMATION:
| APPLICANT: Swanson, Rohert A. APPLICANT: Swanson, Robert A. APPLICANT: Scaleger. Christa | APPLICANT: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION
Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schleger, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REPERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
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2294 EDVIPRGISFS 2304
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Best Local Similarity
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TYPE: PRT
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US-10-034-623-4
US-10-027-806-4
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US-10-02/-801-4

(Sequence 4, Application US/10027801

(Sequence 4, Application US/10027801

(Sequence 4, Application No. US20030054364A1

(SERERAL INFORMATION:

APPLICANT: Swanson, Rohat A.

APPLICANT: Schleper. Christa

(TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

FILE REFERENCE: DCORP. 1002A

(CURRENT APPLICATION NUMBER: US/10/027,801

CURRENT FILING DATE: EARLIER FILING DATE: 1999-09-29

(CURRENT PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-09-29

(NUMBER OF SEQ ID NOS: 123

(SOFTWARE: FastSEQ for Windows Version 3.0

(SEQ ID NO 4

(SEQ ID NO 4

(SEQ ID NO 4

(SEQ ID NO 4

(SEQ ID NO 4)

(SEQ ID NO 4)
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Pred. No. 5.8e+02;
4; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR PILING DATE: 1999-09-29
PRIOR PLING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
TYPE: PAT
ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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Best Local Similarity 54.5'
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2294 EDVIPRGISFS 2304
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2294 EDVIPRGISFS 2304
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Best Local Similarity 54.5
Matches 6; Conservative
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Sequence 2, Application US/09935290

; Sequence 2, Application US/09935290

; Publication No. US20030044948A1

; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVERNION: 56919, A NOVEL HUMAN ACYLTRANSFERASE AND USES THEREOF
; FILER REFERENCE: MNI-186
; CURRENT APPLICATION NUMBER: US/09/935,290
; CURRENT FILING DATE: 2001-08-21
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 2
; LENGTH: 828
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US-09-778-927A-53

i Sequence 53, Application US/09778927A

j Sequence 53, Application US/09778927A

j Sequence 53, Application US/09778927A

j Sequence 54, Application US20020068342A1

j GENERAL INFORMATION:

j APPLICANT: KHOSRAVI, Rami et al.

j TITLE OF INVENTION: UVARIANTS OF ALTERNATIVE SPLICING

j TITLE OF INVENTION: UVARIANTS OF ALTERNATIVE SPLICING

j TILE OF INVENTION: UVARIANTS OF ALTERNATIVE SPLICING

j FILE REFREENCE: 2786-0160P

j CURRENT FILING DATE: 2001-02-08

j PRIOR APPLICATION NUMBER: IL 134453

j PRIOR FILING DATE: 2000-02-09

j PRIOR FILING DATE: 2000-02-09

j PRIOR FILING DATE: 2000-03-29

j NUMBER OF SEQ ID NOS: 81

j SEQ ID NO 53

LENGTH: 254
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62.5%; Pred. No. 1.9e+02;
tive 3; Mismatches 0;
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6675
LENGTH: 332
                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6675
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 75.0 Matches 6; Conservative
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Matches 5; Conservative
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ORGANISM: Homo sapiens
PEATURE:
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118 VLPVGMAY 125
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ORGANISM: Homo sapiens
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APPLICANT: Field, Loren J.
APPLICANT: Field, Loren J.
APPLICANT: Pasumarthi, Kishore Babu S.
ITILE OF INVENTION: CARDIOMYCOTTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
ITILE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT APPLICATION NUMBER: 00/139,942
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
FIREMALIANCE PATENTING DATE: 2000-06-19
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Patent No. US20020166134A1

GENERAL INFORMATION:

APPLICANT: Field, Loren J.

APPLICANT: Field, Loren J.

APPLICANT: Fasumarthi, Kishore Babu S.

TITLE OF INVENTION: CARDIOMYCCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

FILE REFERENCE: 7037-450

CURRENT APPLICATION NUMBER: 60/139,942

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 2000-06-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 289
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                                                                                                                                                    Gaps
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                                                                                                      61.8%; Score 34; DB 10; Length 254; 60.0%; Pred. No. 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 9; Length 289;
Pred. No. 95;
; NAME/KEY: misc_feature
; LOCATION: (1)...(254)
; CTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-527A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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60.0%;
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Best Local Similarity 60.0%
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CORGANISM: Homo sapiens
US-10-024-066-4
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ORGANISM: Mus musculus
                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
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US-10-024-066-4
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US-09-919-497-54
is Sequence 54, Application US/09919497
; Sequence 54, Application US/09919497
; General No. US20020106662A1
; GENERAL INFORMATION:
; APPLICATION: MITTER GOODS INCOMPTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER; FILE REFERENCE: B0001/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT PILING DATE: 2001-07-31
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 54
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Publication No. US20030022199A1

GENERAL INFORMATION:
APPLICANT: Nozu, Jun.IChi
APPLICANT: TSUJi, Akira
APPLICANT: TSUJi, Akira
CURENT APPLICATION
CURRENT APPLICATION NUMBER: US/10/101,921

CURRENT FILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-21

NUMBER: OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 691
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  2; Indels
  2; Mismatches
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Matches 6; Conservative
  6; Conservative
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74 EEVFPLAMNY 83
                                        1 EEVVPVGMSY 10
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                                                                          74 EEVFPLAMNY 83
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US-10-101-921-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-919-497-54
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188 IVPLGLSY 195
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US-09-925-731-2
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US-10-101-921-4
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223 EFVIPAGOSY 232
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US-10-214-766-43
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Publication No. US20030092124A1
GENERAL INFORMATION:
APPLICANT: Cravchic, Anibal
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING GPCR.PROTEINS, AND USES
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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62.5%; Pred. No. 2.4e+02;
tive 3; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/270,333
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/175,691
PRIOR APPLICATION NUMBER: 60/175,691
PRIOR PLING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/191,638
PRIOR PLING DATE: 2000-03-23
PRIOR PLING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
                APPLICANT: ADEOKON, ANTHONI MONISOLA
APPLICANT: AMBROSE, HELEN JEAN
APPLICANT: CRESSWELL, CARL JOHN
TITLE OF INVENTION: CHEMICAL COMPOUNDS
FILE REFERENCE: DJ8/009901/0282795
CURRENT APPLICANTON NUMBER: US/09/925,731
CURRENT APPLICATION NUMBER: 60/226,909
PRIOR PILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-08-23
WUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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; Sequence 66, Application US/09947387
; Patent No. US20020150885A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cal, Sul Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62...
5, Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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188 IVPLGLSY 195
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GENERAL INFORMATION:
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LENGTH: 691
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LENGTH: 774
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TITLE OF INVENTION: No. US20020150885Alel Fluorogenic or Fluorescent Reporter Molecult TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: Use Thereof File REFERENCE: 1735.029005

CURRENT APPLICATION NUMBER: US/09/947,387

CURRENT PILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: US 60/061,582

PRIOR FILING DATE: 1997-10-10

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1998-03-03

PRIOR FILING DATE: 1998-10-09

NUMBER OF SEQ ID NOS: 142

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 66
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TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
FILE REFERENCE: CA1138
CURRENT APPLICATION NUMBER: US/10/214,766
CURRENT PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,734
PRIOR APPLICATION NUMBER: US 60/311,734
PRIOR PILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.2
LENGTH: 426
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.052.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.0%; Score 33; DB 10; Length 10; Best Local Similarity 50.0%; Pred. No. 3.9; Matches 5; Conservative 3; Mismatches 2; Indels
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60.0%; Score 33; DB 9; I
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 43, Application US/10214766; Publication No. US20030084473A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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audet-909-4.rapb

Page 5

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0; Gaps
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PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 108
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-09-924-340-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 4, 2003, 13:30:39 Job time: 14.25 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 4, 2003, 13:09:19; Search time 9.75 Seconds (without alignments) 33.195 Million cell updates/sec

AUDET-909-4 55 1 eevvpvgmsys 11

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 segs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:\*

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cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

cgn2\_6/ptodata/1/iaa/PacKfiles1.pep:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
Н	35	63.6	45	5	-637~759B-23	
61	35	63.6	45	m	Å	e 236,
m	35	63.6	45	4		e 236
4	34	61.8	102	~	US-08-580-988A-23	e 23, 7
Ŋ	34	61.8	152	0	US-08-460-694-4	4,
9	34	61.8	152	ო	US-08-460-744-4	4
7	34	61.8	152	m		4
80	34		173		US-08-193-977-7	7
σ	34		189	N		Sequence 21, Appl
10	34			7	US-08-246-361A-21	21
11	34			m	US-08-463-772-21	e 21
12	34	61.8		S	PCT-US93-05000-21	21
13	34			7	US-08-464-517-22	22
14	34			~	US-08-246-361A-22	22
15	34	61.8		ო	US-08-463-772-22	22
16	34			ß	PCT-US93-05000-22	22
17	34			~	-08-464	9
18	34			m	US-08-463-772-6	é,
19	34			7	US-08-246-361A-4	4,
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21	34			ß	PCT-US93-05000-6	ý,
22	34			7	US-08-464-517-23	23
23	34			7	US-08-246-361A-6	6
24	34	61.8		7	US-08-246-361A-23	23
25	34	61.8		m	US-08-463-772-23	23
26	34	61.8	292	Ŋ	PCT-US93-05000-23	23,
. 27	34	61.8	295	ч	US-07-947-120-8	Sequence 8, Appli

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0; Gaps

Query Match 63.6%; Score 35; DB 2; Length 45; Best Local Similarity 60.0%; Pred. No. 3.6; Matches 6; Conservative 2; Mismatches 2; Indels

Sequence 8, Appli Sequence 2, Appli	19,	Sequence 19, Appl	Sequence 20, Appl	Sequence 19, Appl	2, A	Sequence 2, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 19, Appl	Sequence 20, Appl	Sequence 4, Appli	Seguence 4, Appli	Sequence 3, Appli	Sequence 8, Appli
US-08-472-893A-8 US-08-460-694-2	US-08-464-517-19	US-08-181-317-20	US-08-246-361A-20	US-08-463-772-13	US-08-460-744-2	US-07-667-711B-2	US-08-947-492-8	PCT-US93-05000-2	PCT-US93-05000-19	PCT-US93-05000-20	US-08-464-517-4	US-08-463-772-4	US-08-770-761A-3	US-08-770-761A-8
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295 295	295	295	295	299	295	295	295	295	295	295	309	309	618	647
61.8 61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8
34 34	34	3 4	34	3 6	34	34	34	34	34	34	34	34	34	34
7 N 7 N	30	35	33		36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

7759B en, ation of Genes enter Street \$1.0, Version #1. 37,759B \$/02875	
TELECOMMUNICATION INFORMATION: TELEPROSE (404) 873-8794 TELEPRAX: (404) 873-8795 TELEPRAX: (404) 873-8795 TELEPRAX: (404) 873-8795 INFORMATION FOR SEQ ID NO: 236: SEQUENCE CHARACTERISTICS: LENGTH: 45 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear MOLECTLE TYPE: protein HYPOTHETICAL: NO US-08-637-7598-236	

audet-909-4.rai

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NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: RPMS 101 CON
TATORNEY/AGENT INFORMATION:
NAME: PABLE, PARLYER 1.
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: RPMS 101 CON
TELECOMMUNICATION NUMBER: RPMS 101 CON
TELECOMMUNICATION NUMBER: RPMS 101 CON
TELECOMMUNICATION S73-8794
INFORMATION FOR SEQ 1D NO: 236:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-201-945-236
; Sequence 236, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
                                                                                                                                                  Sequence 236, Application US/08871355A
Patent No. 601569
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
TITLES ONDERSSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0°
EEVVPVGMSY 10
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EEISPLGWSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                      Georgia

    CITY: Atlanta

                                                                                                                                US-08-871-355A-236
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%Sequence 23, Application US/08580988A

; Sequence 23, Application US/08580988A
; Sequence 23, Application US/08580988A
; Patent No. 58561B
; STATES OF INFORMATION:
    TITLE OF INVENTION: Tumor Necrosis Factor
    TITLE OF INVENTION: For Its Use
    TITLE OF INVENTION: For Its Use
    NUMBER OF SEQUENCES: 27
    CORRESPENDENCE ADDRESS:
    ADDRESSEE: Dr. Benjamin A. Adler
    STREET: B011 Candle Lane
    CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No. 3.6;
2; Mismatches 2; Indels
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Morosoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benjamin Aaron Adler, Ph.D., J.D.
                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PROST. PATER L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: January 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.6%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.6
Best Local Similarity 60.0
Matches 6; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEVVPVGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                    30309-3450
Georgia
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                                                                                                                                                                                                                                                                                                            FILING DATE:
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STATE: Te
COUNTRY:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   61.8%; Score 34; DB 2; Length 102; 60.0%; Pred. No. 14; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD! Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESSEDNDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
AURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
35,423
MER: D5721CIP2
REGISTRATION NUMBER: 35,423
REPERENCE/DOCKET NUMBER: D572
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEPHONE: 713-777-2321
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                            Ylex...
TOPOLOGY: linea.
MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                             no
PR: internal
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-460-694-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EEVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| |: |:|
24 EEVFPLAMNY 33
                                                                                                                                                                                                                                                                                           ANTI-SENSE: no
FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                            US-08-580-988A-23
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US-08-460-694-4
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1 EEVVPVGMSY 10

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Gaps
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                                                                                                                           Sequence 4, Application US/08460744

Patent No. 6107541

GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INFORMATION: Pradi Cyclin and Its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSED: STERNE, KESSIER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILLING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIF: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EEVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                          20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-667-711B-4
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                          RESULT 6
US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-460-744-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
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Gaps ; 0

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2; Indels
      Pred. No. 27;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-WAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617) 227-5400
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCIII (EAKL)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 189 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.8
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-464-517-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEVVPVGMSY 10
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                                                                                                      1 EEVVPVGMSY 10
                                                                                                                                                                  55 EEVFPLAMNY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                   US-08-464-517-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: M. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: PAPTILCOMAVIEUS B7 ONCOPROTEIN
TITLE OF INVENTION: PAPILLOMAVIEUS B7 ONCOPROTEIN
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 23;
2; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                             APPLICATION DAIR

CARSIN AFFILANCE DAIR

FILING DATE: 11-MAR-1991

ATTORNEY AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811

REGISTRATION NUMBER: 35,811

REFERENCE/DOCKET NUMBER: 0609.4070000

TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600

TELEFAX: (202) 371-2500

TELEFAX: (202) 371-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: REED & ROBINS
1: 635 BRYANT STREET
PALO ALTO
CALIFORNIA
1X: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
INFORMATION FOR SEC ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08193977
Patent No. 5625031
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.8%;
Best Local Similarity 60.0%;
Matches 6; Conservative ;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-07-667-711B-4
             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-193-977-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPVGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 EEVFPLAMNY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-193-977-7
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Sequence 21, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-246-361A-21
; Sequence 21, Application US/08246361A
; Patent No. 599852
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.8%; Score 34; DB 2; Length 189; 60.0%; Pred. No. 29;
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TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-463-772-21
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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PCT-US93-05000-21
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| Squence 21, Application US/08463772
| Patent NO. 6066501
| GENERAL INFORMATION:
| APPLICANT: BEACH, David H.
| TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
| CORRESPONDENCE ADDRESS:
| ADDRESSE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston STREET: MA
| COUNTRY: WA
| COUNTRY: MA
| COUNTRY: RADABLE FORM:
| MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
| CURRENT APPLICATION NUMBER: US/08/463,772
| FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.8%; Score 34; DB 2; Length 189; 60.0%; Pred. No. 29; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                       CURRENT AFPLICATION DATA:

APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
FILING APPLICATION 1435
PRIOR APPLICATION 1435
FILING DATE: 16-OCT-1992
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
FILING DATE: 26-MAY-1992
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATHEW P. VINCENT
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTER/STICS:
                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 189 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                        SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.8°
Best Local Similarity 60.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-21
                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EEVVPVGMSY 10
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                       Abbar-
STREET: bc-
-mv. Boston
                                                                                                   USA
                   ADDRESSEE:
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2; Mismatches
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MEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: 36,709
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEN NUMBER: MII-004C
TELEFRANCE/DOCKET NUMBER: MII-004C
TELEFRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
CENTRALICATERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EEVVPVGMSY 10
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                                                                                                                                                                                    STATE: MA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-246-361A-22
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                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08464517
Sequence 22, Application US/08464517
Sequence 22, Se69640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.8%; Score 34; DB 2; Length 236; 60.0%; Pred. No. 38;
                                                           Score 34; DB 5; Length 189;
Pred. No. 29;
                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/889,178
FILING DATE: 16-MAX-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
TELEPHONE: (617) 227-541
INFORMATION FOR SEQ ID NO: 22:
FUNCHALLY OF ALL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-246-361A-22
; Sequence 22, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
                                                       Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 236 amino acids
amino acid
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Best Local Similarity 60.0°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide US-08-464-517-22
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20 EEVFPLAMNY 29
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                                                                                                                                                                                                                                     74 EEVFPLAMNY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 02109
PCT-US93-05000-21
                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-464-517-22
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Gaps
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Sequence 22, Application US/08463772

Sequence 22, Application US/08463772

PAUGHT NO. 606501

APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: ALAHIVE & COCKFIELD

STREET: 60 State Street
APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 2; Length 236;
Pred. No. 38;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: 36,709
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
FELECOMMUNICATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
RETERENCE/DOCKET NUMBER: 36,709
RETERENCE/DOCKET NUMBER: 36,709
RETERENCE/DOCKET NUMBER: 36,709
RETERENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
ILBUGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
TYPE: amino acids
TYPE: amino acid
TYPE: peptide
US-08-463-772-22
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Search completed: June 4, 2003, 13:14:59 Job time: 9.75 secs

1 EEVVPVGMSY 10 ||| |: |:| 20 EEVFPLAMNY 29

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Gaps

Ouery Match 61.8%; Score 34; DB 3; Length 236; Best Local Similarity 60.0%; Pred. No. 38; Matches 6; Conservative 2; Mismatches 2; Indels

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